

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:15:59 ; Search time 23.86 Seconds

(without alignments)  
139.702 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264  
Sequence: 1 PCGPCSERRKHLFVQDPQC.....NTDSRCKAROLELNEPTCRC 45

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 330423

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq\_1101.\*  
1: /SID8/gcgdata/geneseq/AA1980.DAT.\*  
2: /SID8/gcgdata/geneseq/AA1981.DAT.\*  
3: /SID8/gcgdata/geneseq/AA1982.DAT.\*  
4: /SID8/gcgdata/geneseq/AA1983.DAT.\*  
5: /SID8/gcgdata/geneseq/AA1984.DAT.\*  
6: /SID8/gcgdata/geneseq/AA1985.DAT.\*  
7: /SID8/gcgdata/geneseq/AA1986.DAT.\*  
8: /SID8/gcgdata/geneseq/AA1987.DAT.\*  
9: /SID8/gcgdata/geneseq/AA1988.DAT.\*  
10: /SID8/gcgdata/geneseq/AA1989.DAT.\*  
11: /SID8/gcgdata/geneseq/AA1990.DAT.\*  
12: /SID8/gcgdata/geneseq/AA1991.DAT.\*  
13: /SID8/gcgdata/geneseq/AA1992.DAT.\*  
14: /SID8/gcgdata/geneseq/AA1993.DAT.\*  
15: /SID8/gcgdata/geneseq/AA1994.DAT.\*  
16: /SID8/gcgdata/geneseq/AA1995.DAT.\*  
17: /SID8/gcgdata/geneseq/AA1996.DAT.\*  
18: /SID8/gcgdata/geneseq/AA1997.DAT.\*  
19: /SID8/gcgdata/geneseq/AA1998.DAT.\*  
20: /SID8/gcgdata/geneseq/AA1999.DAT.\*  
21: /SID8/gcgdata/geneseq/AA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	100.0	45	20	VEGF antagonist pe
2	255	96.6	44	14	Encoded by human V
3	255	96.6	44	20	SEQ ID NO. 11 of W
4	250	94.7	44	17	VEGF exon VII. Ho
5	178	67.4	41	21	Immunogenic peptid
6	138	52.3	24	20	VEGF antagonist pe
7	115	43.6	21	17	VEGF antagonist pe
8	115	43.6	55	17	AAW04825
9	115	43.6	55	20	AAW80489
10	76	28.8	20	14	Murine vascular en
11	58	22.0	62	21	Guinea pig VFP C-T
					Arabidopsis thalia

12	58	22.0	62	21	AA643390
13	58	22.0	67	21	AA605269
14	58	22.0	67	21	AA608909
15	58	22.0	67	21	AA643389
16	58	22.0	83	21	AA605267
17	58	22.0	83	21	AA608908
18	58	22.0	83	21	AA643388
19	56.5	21.4	84	22	AAW06548
20	56.5	21.4	89	21	AA632062
21	55	20.8	53	20	AAV01794
22	54	20.5	53	20	AAV01789
23	52.5	19.9	69	22	AA670806
24	52	19.7	68	12	AA614774
25	52	19.7	68	13	AA625720
26	52	19.7	68	15	AA633883
27	51.5	19.5	53	22	AA619878
28	51.5	19.5	53	22	AA633401
29	51.5	19.5	76	22	AAU05927
30	51	19.3	67	22	AA661455
31	50	18.9	49	21	AA636714
32	50	18.9	49	21	AA636716
33	50	18.9	63	21	AA657811
34	50	18.9	69	21	AA641332
35	50	18.9	100	22	AA634792
36	49.5	18.8	63	20	AA659759
37	49	18.6	35	22	AA660793
38	48	18.2	49	17	AAW02648
39	48	18.2	49	21	AA636718
40	48	18.2	53	18	AA634467
41	48	18.2	53	19	AAW50140
42	48	18.2	53	20	AAV01792
43	48	18.2	57	21	AA657813
44	47.5	18.0	26	15	AA653384
45	47.5	18.0	58	22	AA669201

#### ALIGNMENTS

RESULT 1	
AAV22023	standard; peptide; 45 AA.
ID	AAV22023
AC	AAV22023;
XX	
DT	26-AUG-1999 (first entry)
XX	
DE	VEGF antagonist peptide.
XX	
VEGF	vascular endothelial growth factor; antagonist; neovascularisation;
KW	angiogenesis; retinal neovascularisation; haemangioma; Kaposi's sarcoma;
KW	solid tumour growth; leukaemia; metastasis; psoriasis; osteoarthritis;
KW	angiogenic disease; neovascular glaucoma; diabetic retinopathy; therapy;
KW	rheumatoid arthritis; endometriosis; muscular degeneration;
XX	
OS	Homo sapiens.
XX	
PN	W09929861-A1.
XX	
PD	17-JUN-1999.
XX	
PF	09-DEC-1998; 98MO-US26103.
XX	
PR	12-DEC-1997; 97US-0069687.
XX	
PR	09-DEC-1997; 97US-0069155.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX	
PI	Klagsbrun M, Soker S;
XX	
DR	WPI; 1999-385607/32.
XX	

PT New peptide antagonists of vascular endothelial growth factor (VEGF)  
 XX  
 PS Claim 1: Page 46; 53pp; English.  
 XX  
 CC This sequence represents a vascular endothelial growth factor (VEGF)  
 CC antagonist of the invention. The antagonist is a portion of the seventh  
 CC exon of VEGF, and acts as an antagonist to all VEGF isoforms, even if  
 CC they do not have exon 7. The VEGF antagonist peptides can be used to  
 CC treat diseases or disorders associated with VEGF-induced  
 CC neovascularisation or inappropriate angiogenesis. Diseases and disorders  
 CC treated include retinal neovascularisation, haemangiomas, solid tumour  
 CC growth, leukaemia, metastasis, psoriasis, neovascular glaucoma, diabetic  
 CC retinopathy, rheumatoid arthritis, osteoarthritis, endometriosis,  
 CC muscular degeneration, and retinopathy of prematurity (ROP), and Kaposi's  
 CC sarcoma. Solid tumours expressing VEGF are also a target for gene  
 CC therapy using the peptide antagonist of the invention, e.g. neoplasms of  
 CC the central nervous system (glioblastomas, astrocytomas, neuroblastomas,  
 CC meningiomas, ependymomas), cancers of hormone-dependent tissues (e.g.  
 CC prostate, testicles, uterus, ovary, mammary carcinoma), melanomas,  
 CC cancers of the lung, and cancers of the gastrointestinal tract. Current  
 CC treatment of angiogenic diseases is inadequate. Although preliminary  
 CC results with antiangiogenic proteins are promising, the proteins are  
 CC relatively large in size and so are difficult to use and produce.  
 CC Antiangiogenic agents that show improvement in size, ease of production,  
 CC stability and/or potency would be desirable. The peptides of the  
 CC invention go some way to achieving these aims.  
 XX  
 SQ Sequence 45 AA;

Query Match 100.0%; Score 264; DB 20; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-22;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PCGPGSRKHLFYQDPQTCCKSCKNMDSRCKARQLEINERTC 45  
 DB 1 pcgpgserkhltyqdpqtcckscnldsrckarqleinertrc 45

RESULT 2  
 AAR42613  
 ID AAR42613 standard; Protein; 44 AA.  
 XX  
 AC AAR42613;  
 XX  
 DT 28-OCT-1993 (first entry)  
 XX  
 DE Encoded by human VEGF-165 exon VII.  
 XX  
 KW Angiogenesis; wound healing; mitogen; vascular endothelial cells;  
 KW Vascular Endothelial Cell Growth Factor; hVEGF-165; hVEGF-121;  
 KW alternative RNA splicing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5219739-A.  
 XX  
 PD 15-JUN-1993.  
 XX  
 PF 27-JUL-1989; 89US-0387545.  
 XX  
 PR 27-JUL-1989; 89US-0387545.  
 PR 14-DEC-1989; 89US-0450883.  
 PR 27-JUL-1990; 90US-0559041.  
 XX  
 PA (SCIO-) SCTOS NOVA INC.  
 XX  
 PI Abraham JA, Fiddes JC, Mitchell RL, Fischer EG;  
 XX  
 DR MPI: 1993-205302/25.  
 DR N-PSDB; AAQ49609.  
 XX  
 PT Isolated DNA sequences, expression vectors and transformant cells

PT - used for large scale prodn. of vascular endothelial cell growth  
 PT factor, for treating wounds in which neo-vascularisation is  
 PT required  
 XX  
 PS Claim 8; Fig 8; 40pp; English.  
 XX  
 CC The sequences of the 8 possible exons encoding human vascular  
 CC endothelial cell growth factor, together with contiguous splice  
 CC junctions, were obtained from overlapping genomic inserts. A method  
 CC for producing VEGF is claimed comprising culturing mammalian cells  
 CC transformed with an expression vector containing exons I-V and  
 CC VIII. See AAQ44261 for exon I and AAQ45604-Q49610 for exons II-VIII.  
 XX  
 SQ Sequence 44 AA;

Query Match 96.6%; Score 255; DB 14; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-21;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PCGPGSRKHLFYQDPQTCCKSCKNMDSRCKARQLEINERTC 44  
 DB 1 pcgpgserkhltyqdpqtcckscnldsrckarqleinertrc 44

RESULT 3  
 AAY23249  
 ID AAY23249 standard; Protein; 44 AA.  
 XX  
 AC AAY23249;  
 XX  
 DT 31-AUG-1999 (first entry)  
 XX  
 DE SEQ ID NO. 11 of WO930157.  
 XX  
 KW Cancer; vascular endothelial growth factor receptor; VEGF receptor;  
 KW neuropilin; NP-1; NP-2; metastatic potential; malignant cell;  
 KW breast cancer; prostate cancer; ischemia; gene therapy;  
 KW angiogenesis; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO930157-A2.  
 XX  
 PD 17-JUN-1999.  
 XX  
 PE 09-DEC-1998; 98WO-US26127.  
 XX  
 PR 12-DEC-1997; 97US-0069687.  
 PR 09-DEC-1997; 97US-0069155.  
 XX  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 XX  
 PI Klagsbrun M, Miao H, Soker S, Takashima S;  
 XX  
 DR MPI: 1999-395021/33.  
 XX  
 PT Diagnosis and prognosis of cancer using vascular endothelial growth  
 PT factor receptors  
 XX  
 PS Disclosure; Page 80; 82pp; English.  
 XX  
 CC The specification describes methods for the diagnosis and prognosis of  
 CC cancer using vascular endothelial growth factor (VEGF) receptors  
 CC (neuropilins) such as VEGFR165R/NP-1 and NP-2 which are associated with  
 CC metastatic potential of a malignant cell. The methods can be used for  
 CC the diagnosis and prognosis of cancer, especially breast and prostate  
 CC cancer. DNA encoding VEGFR165R/NP-1 or NP-2 can be used to treat  
 CC ischemia, e.g. heart and limb. The DNA can also be used as an adjunct  
 CC to gene therapy with VEGF. The VEGFR165R/NP-1 or NP-2 proteins can be  
 CC used to identify antagonists and agonists, which can be used to  
 CC inhibit angiogenesis, and metastasis in malignant cells. Antibodies  
 CC directed against VEGFR165R/NP-1 or NP-2 proteins can also be used for

CC the treatment or prophylaxis of cancers. The present sequence is  
 CC used in the course of the invention.

XX  
 SQ Sequence 44 AA;

Query Match 96.6%; Score 255; DB 20; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-21;  
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PCGPGSERRRKHLFVODPOTCKSCCKMTDSRCKAROLELNERTC 44  
 Db 1 pcgpgserrrkhlfvodpqtckscckmtdsrckarqlelnertr 44

#### RESULT 4

AA94041  
 ID - AA94041 standard; Protein; 44 AA.

XX  
 AC AA94041;

XX  
 DT 10-OCT-1996 (first entry)

XX  
 DE VEGF exon VII.

XX Vascular endothelial growth factor; VEGF; human; conjugate; tumour; iris;  
 KW proliferation inhibition; VEGF-mediated pathophysiological condition;  
 KW dermatological disorder; VEGF receptor; vascular proliferation; retina;  
 KW ophthalmic disorder; hyperproliferating blood vessel; therapy; psoriasis;  
 KW conjunctiva; vitreous humour; rheumatoid arthritis; skin cancer;  
 KW varicose veins; gene therapy.

XX  
 OS Homo sapiens.

XX  
 PN MO9606641-A1.

XX  
 PD 07-MAR-1996.

XX  
 PF 29-AUG-1995; 95WO-US10973.

XX  
 PR 16-MAY-1995; 95US-0441979.

XX  
 PR 29-AUG-1994; 94US-0297961.

XX  
 PA (PRIZ-) PRIZM PHARM INC.

XX  
 PI Fleurbailj GA, Freund E, Houston LL, Nova MP, Sosnowski BA;

XX  
 PI Victor KD;

XX  
 DR WPI; 1996-160151/16.

XX  
 DR N-PSDB; AAT17749.

XX  
 PT Vascular endothelial cell growth factor (VEGF) conjugates - having

XX  
 PT VEGF linked to targeted agent, used for inhibiting proliferation of

XX  
 PT cells, e.g. for gene therapy

XX  
 PS Disclosure; Page 121; 193pp; English.

XX  
 PS AAR94033-R94038, AAR94041, AAR94042 and AAM00582 represent vascular

XX  
 CC endothelial growth factors (VEGF) exons. This sequence represents exon

XX  
 CC VII. These sequences were used in VEGF conjugates of the invention. In

XX  
 CC the conjugates, VEGF (or fragments of it) are linked to a targeted agent

XX  
 CC (this can be via a linker sequence), so that the conjugate binds to a

XX  
 CC VEGF receptor. Cys-modified forms of VEGF are particularly suitable for

XX  
 CC chemical conjugation to linkers and targeted agents. The conjugates are

XX  
 CC used for inhibiting proliferation of cells bearing VEGF receptors. They

XX  
 CC can be used for treating a VEGF-mediated pathophysiological condition,

XX  
 CC including dermatological disorders with underlying vascular

XX  
 CC proliferation, solid tumours or an ophthalmic disorder of

XX  
 CC hyperproliferating blood vessels of the retina, iris, conjunctiva or

XX  
 CC vitreous humour. The conjugates can also be used for treating

XX  
 CC psoriasis, rheumatoid arthritis, skin cancers and other tumours, or

XX  
 CC varicose veins. They are also suitable for use in gene therapy.

SQ Sequence 44 AA;

Query Match 94.7%; Score 250; DB 17; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PCGPGSERRRKHLFVODPOTCKSCCKMTDSRCKAROLELNERTC 43  
 Db 1 pcgpgserrrkhlfvodpqtckscckmtdsrckarqlelnertr 43

#### RESULT 5

AA18547  
 ID AA18547 standard; peptide; 41 AA.

XX  
 AC AA18547;

XX  
 DT 15-JAN-2001 (first entry)

XX  
 DE Immunogenic peptide fragment derived from FGF and/or VEGF.

XX Immunogenic peptide; fibroblast growth factor; FGF; VEGF; cancer;  
 KW vascular endothelial growth factor; hyperproliferative disorder;  
 KW haemangioma; solid tumour; blood borne tumour; leukaemia; metastasis;  
 KW telangiectasia; psoriasis; scleroderma; pyogenic granuloma;  
 KW myocardial anglogenesis; Crohn's disease; plaque neovascularisation;  
 KW arteriovenous malformation; corneal disease; rubecosis;  
 KW neovascular glaucoma; diabetic retinopathy; retrolental fibroplasia;  
 KW arthritis; diabetic neovascularisation; macular degeneration;  
 KW wound healing; peptic ulcer; Helicobacter related disease; fracture;  
 KW keloid; vasculogenesis; hematopoiesis; ovulation; menstruation;  
 KW placentalion; cat scratch fever.

XX  
 OS Unidentified.

XX  
 PN WO200053219-A2.

XX  
 PD 14-SEP-2000.

XX  
 PF 10-MAR-2000; 2000MO-US06320.

XX  
 PR 11-MAR-1999; 99US-0266543.

XX  
 PA (ENTR-) ENTREMED INC.

XX  
 PI Holaday JW, Ruiz A, Madsen J;

XX  
 PI WPI; 2000-594263/56.

XX  
 DR WPI; 2000-594263/56.

XX  
 DR N-PSDB; AAT17749.

XX  
 PT An immunogenic composition useful for treating cancer or

XX  
 PT hyperproliferative disorders comprises an immunogenic peptide fragment

XX  
 PT of fibroblast growth factor and/or vascular endothelial growth factor -

XX  
 PS Claim 13; Page 28; 95pp; English.

XX  
 PS AAB18542-51 represent immunogenic peptide fragments of fibroblast

XX  
 CC growth factor (FGF) and/or vascular endothelial growth factor (VEGF).

XX  
 CC The peptides are used to produce immunogenic compositions. The

XX  
 CC immunogenic composition is used for treating cancer or

XX  
 CC hyperproliferative disorders, especially haemangioma, solid tumours,

XX  
 CC blood borne tumours, leukaemia, metastasis, telangiectasia, psoriasis,

XX  
 CC scleroderma, pyogenic granuloma, myocardial anglogenesis, Crohn's

XX  
 CC disease, plaque neovascularisation, arteriovenous malformations,

XX  
 CC corneal diseases, rubecosis, neovascular glaucoma, diabetic retinopathy,

XX  
 CC retrolental fibroplasia, arthritis, diabetic neovascularisation, macular

XX  
 CC degeneration, wound healing, peptic ulcer, Helicobacter related

XX  
 CC diseases, fractures, keloids, vasculogenesis, hematopoiesis, ovulation,

XX  
 CC menstruation, placentalion and cat scratch fever.

XX  
 SQ Sequence 41 AA;

Query Match 67.4%; Score 178; DB 21; Length 41;  
Best Local Similarity 89.7%; Pred. No. 9.4e-13;  
Matches 35; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

Oy 7 ERKHLFQDPQTCCKSCKNTDSRCARQLEINERTCRC 45  
Db 2 erkhlly--qtckscskldsrcrkqle-nertrc 36

RESULT 6

AAV22024  
ID AAV22024 standard; peptide: 24 AA.

AC AAV22024;

DT 26-AUG-1999 (first entry)

DE VEGF antagonist peptide.

XX VEGF: vascular endothelial growth factor; antagonist; neovascularisation;

KW angiogenesis; retinal neovascularisation; haemangioma; Kaposi's sarcoma;

KW solid tumour growth; leukemia; metastasis; psoriasis; osteoarthritis;

KW angiogenic disease; neovascular glaucoma; diabetic retinopathy; therapy;

KW rheumatoid arthritis; endometriosis; muscular degeneration;

KW retinopathy of prematurity.

XX Homo sapiens.

OS

PN W09929861-A1.

PD 17-JUN-1999.

XX 09-DEC-1998; 98WO-US26103.

XX 12-DEC-1997; 97US-0069687.

PR 09-DEC-1997; 97US-0069155.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Klagsbrun M, Soker S;

DR WPI; 1999-385607/32.

XX New peptide antagonists of vascular endothelial growth factor (VEGF)

PS Claim 2; Page 46; 53pp: English.

XX This sequence represents a vascular endothelial growth factor (VEGF)

CC antagonist of the invention. The antagonist is a portion of the seventh

CC exon of VEGF, and acts as an antagonist to all VEGF isoforms, even if

CC they do not have exon 7. The VEGF antagonist peptides can be used to

CC treat diseases or disorders associated with VEGF-induced

CC neovascularisation or inappropriate angiogenesis. Diseases and disorders

CC treated include retinal neovascularisation, haemangiomas, solid tumour

CC growth, leukemia, metastasis, psoriasis, neovascular glaucoma, diabetic

CC retinopathy, rheumatoid arthritis, osteoarthritis, endometriosis,

CC muscular degeneration, and retinopathy of prematurity (ROP), and Kaposi's

CC sarcoma. Solid tumours expressing VEGF are also a target for gene

CC therapy using the peptide antagonist of the invention, e.g. neoplasms of

Query Match 52.3%; Score 138; DB 20; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 CSCKNTDSRCARQLEINERTCRC 45  
Db 1 cskntdsrckarqleinertrc 24

RESULT 7

AAV22025  
ID AAV22025 standard; peptide: 21 AA.

AC AAV22025;

DT 26-AUG-1999 (first entry)

DE VEGF antagonist peptide.

XX VEGF: vascular endothelial growth factor; antagonist; neovascularisation;

KW angiogenesis; retinal neovascularisation; haemangioma; Kaposi's sarcoma;

KW solid tumour growth; leukemia; metastasis; psoriasis; osteoarthritis;

KW angiogenic disease; neovascular glaucoma; diabetic retinopathy; therapy;

KW rheumatoid arthritis; endometriosis; muscular degeneration;

KW retinopathy of prematurity.

XX Homo sapiens.

OS

PN W09929861-A1.

PD 17-JUN-1999.

XX 09-DEC-1998; 98WO-US26103.

XX 12-DEC-1997; 97US-0069687.

PR 09-DEC-1997; 97US-0069155.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Klagsbrun M, Soker S;

DR WPI; 1999-385607/32.

XX New peptide antagonists of vascular endothelial growth factor (VEGF)

PS Claim 3; Page 46; 53pp: English.

XX This sequence represents a vascular endothelial growth factor (VEGF)

CC antagonist of the invention. The antagonist is a portion of the seventh

CC exon of VEGF, and acts as an antagonist to all VEGF isoforms, even if

CC they do not have exon 7. The VEGF antagonist peptides can be used to

CC treat diseases or disorders associated with VEGF-induced

CC neovascularisation or inappropriate angiogenesis. Diseases and disorders

CC treated include retinal neovascularisation, haemangiomas, solid tumour

CC growth, leukemia, metastasis, psoriasis, neovascular glaucoma, diabetic

CC retinopathy, rheumatoid arthritis, osteoarthritis, endometriosis,

CC muscular degeneration, and retinopathy of prematurity (ROP), and Kaposi's

CC sarcoma. Solid tumours expressing VEGF are also a target for gene

CC therapy using the peptide antagonist of the invention, e.g. neoplasms of



Db 9 cpctctgrgrf---pdprrcrrrrrrflhcgqgglelnptcrrc 50

## RESULT 10

AAR36680

ID AAR36680 standard; peptide: 20 AA.

XX AAR36680;

XX 23-AUG-1993 (first entry)

XX Guinea pig VPF C-terminal.

XX Vascular permeability factor; effusion; malignancy; antibody;

KW guinea pig; human.

XX Cavia porcellus.

XX WO9308473-A.

XX 29-APR-1993.

XX 21-OCT-1992; 92WO-US09068.

XX 24-OCT-1991; 91US-0782350.

XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX Dvorak HF, Yeo K, Yeo T;

XX WPI; 1993-152625/18.

XX Immunopassay for detecting vascular permeability (VPF) factor in  
PT effusions - comprises detecting VPF in sample using immobilised  
PT antibody to C-terminus of VPF having specified sequence and 2nd  
XX labelled antibody to N-terminus

XX Claim 8; Page 20; 33pp; English.

XX An assay method for determining whether an effusion sample obtd.  
CC from a human patient is associated with a malignancy, comprises  
CC measuring VPF in the sample, a VPF level greater than a  
CC predetermined amts. indicates a likelihood that the sample is a  
CC malignant effusion. More specifically, the assay is carried out  
CC with an immobilised first antibody to the C-terminus of guinea pig  
CC VPF (AAR36680) and a second labelled antibody to the N-terminus of  
CC human VPF (AAR36679). The label is pref. a Europium chelate. A level  
CC of more than 30 units indicates a malignant effusion.

XX Sequence 20 AA;

Query Match 28.8%; Score 76; DB 14; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 KAROLELNEPTCRC 45

Db 2 karqelelnertcrrc 15

## RESULT 11

AAG08910

ID AAG08910 standard; Protein: 62 AA.

XX AAG08910;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 6631.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 04-MAY-1999; 99US-0132048.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 18-MAY-1999; 99US-0134370.

XX 19-MAY-1999; 99US-0134768.

XX 20-MAY-1999; 99US-0135941.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 21-JUN-1999; 99US-0139767.

XX 22-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.



PD 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123380.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138847.  
PR 10-JUN-1999; 99US-0139119.  
PR 14-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140595.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 20-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 21-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 06-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.



PR 23-SEP-1999: 99US-0155486.  
PR 24-SEP-1999: 99US-0153659.  
PR 28-SEP-1999: 99US-0156458.  
PR 29-SEP-1999: 99US-0156596.  
PR 04-OCT-1999: 99US-0157117.  
PR 05-OCT-1999: 99US-0157753.  
PR 06-OCT-1999: 99US-0157865.  
PR 07-OCT-1999: 99US-0158029.  
PR 08-OCT-1999: 99US-0158232.  
PR 12-OCT-1999: 99US-0158369.  
PR 13-OCT-1999: 99US-0159293.  
PR 13-OCT-1999: 99US-0159294.  
PR 13-OCT-1999: 99US-0159295.  
PR 14-OCT-1999: 99US-0159329.  
PR 14-OCT-1999: 99US-0159330.  
PR 14-OCT-1999: 99US-0159331.  
PR 14-OCT-1999: 99US-0159637.  
PR 14-OCT-1999: 99US-0159638.  
PR 18-OCT-1999: 99US-0159584.  
PR 21-OCT-1999: 99US-0160741.  
PR 21-OCT-1999: 99US-0160767.  
PR 21-OCT-1999: 99US-0160768.  
PR 21-OCT-1999: 99US-0160770.  
PR 21-OCT-1999: 99US-0160814.  
PR 21-OCT-1999: 99US-0160815.  
PR 22-OCT-1999: 99US-0160980.  
PR 22-OCT-1999: 99US-0160981.  
PR 22-OCT-1999: 99US-0160989.  
PR 25-OCT-1999: 99US-0161404.  
PR 25-OCT-1999: 99US-0161405.  
PR 25-OCT-1999: 99US-0161406.  
PR 26-OCT-1999: 99US-0161359.  
PR 26-OCT-1999: 99US-0161360.  
PR 26-OCT-1999: 99US-0161361.  
PR 28-OCT-1999: 99US-0161920.  
PR 28-OCT-1999: 99US-0161892.  
PR 28-OCT-1999: 99US-0161993.  
PR 29-OCT-1999: 99US-0162142.

Query Match Best Local Similarity 22.0%: Score 58; DB 21; Length 62;

Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

QY 7 ERRKHLFVDPQTCCKSCNKTDSCKARQLELNERTC--RC 45  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 eyrvelfnktaqcfnc--vdkrkykaealmngenscidtc 40

RESULT 13

AG05269 ID AAG05269 standard; Protein; 67 AA.

XX AC AAG05269;

XX DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 1611.

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999: 99US-0121825.

PR 05-MAR-1999: 99US-0123180.

PR 09-MAR-1999: 99US-0123548.

PR 22-MAR-1999: 99US-0125788.  
PR 25-MAR-1999: 99US-0126264.  
PR 29-MAR-1999: 99US-0126785.  
PR 01-APR-1999: 99US-0127462.  
PR 06-APR-1999: 99US-0128234.  
PR 08-APR-1999: 99US-0128714.  
PR 16-APR-1999: 99US-0129845.  
PR 19-APR-1999: 99US-0130077.  
PR 21-APR-1999: 99US-0130449.  
PR 23-APR-1999: 99US-0130510.  
PR 23-APR-1999: 99US-0130891.  
PR 28-APR-1999: 99US-0131449.  
PR 30-APR-1999: 99US-0132048.  
PR 30-APR-1999: 99US-0132407.  
PR 04-MAY-1999: 99US-0132484.  
PR 05-MAY-1999: 99US-0132485.  
PR 06-MAY-1999: 99US-0132486.  
PR 06-MAY-1999: 99US-0132487.  
PR 07-MAY-1999: 99US-0132863.  
PR 11-MAY-1999: 99US-0134256.  
PR 14-MAY-1999: 99US-0134218.  
PR 14-MAY-1999: 99US-0134219.  
PR 14-MAY-1999: 99US-0134221.  
PR 14-MAY-1999: 99US-0134370.  
PR 18-MAY-1999: 99US-0134768.  
PR 19-MAY-1999: 99US-0134941.  
PR 20-MAY-1999: 99US-0135124.  
PR 21-MAY-1999: 99US-0135353.  
PR 22-MAY-1999: 99US-0135629.  
PR 25-MAY-1999: 99US-0136021.  
PR 27-MAY-1999: 99US-0136392.  
PR 28-MAY-1999: 99US-0136782.  
PR 01-JUN-1999: 99US-0137222.  
PR 03-JUN-1999: 99US-0137528.  
PR 04-JUN-1999: 99US-0137724.  
PR 07-JUN-1999: 99US-0138094.  
PR 08-JUN-1999: 99US-0138540.  
PR 10-JUN-1999: 99US-0138847.  
PR 14-JUN-1999: 99US-0139119.  
PR 16-JUN-1999: 99US-0139452.  
PR 16-JUN-1999: 99US-0139453.  
PR 17-JUN-1999: 99US-0139494.  
PR 18-JUN-1999: 99US-0139454.  
PR 18-JUN-1999: 99US-0139455.  
PR 18-JUN-1999: 99US-0139456.  
PR 18-JUN-1999: 99US-0139457.  
PR 18-JUN-1999: 99US-0139458.  
PR 18-JUN-1999: 99US-0139459.  
PR 18-JUN-1999: 99US-0139460.  
PR 18-JUN-1999: 99US-0139461.  
PR 18-JUN-1999: 99US-0139462.  
PR 18-JUN-1999: 99US-0139463.  
PR 18-JUN-1999: 99US-0139750.  
PR 18-JUN-1999: 99US-0139763.  
PR 21-JUN-1999: 99US-0139817.  
PR 22-JUN-1999: 99US-0139899.  
PR 23-JUN-1999: 99US-0140353.  
PR 23-JUN-1999: 99US-0140354.  
PR 24-JUN-1999: 99US-0140695.  
PR 24-JUN-1999: 99US-0140823.  
PR 29-JUN-1999: 99US-0140991.  
PR 30-JUN-1999: 99US-0141287.  
PR 01-JUL-1999: 99US-0141842.  
PR 01-JUL-1999: 99US-0142154.  
PR 02-JUL-1999: 99US-0142055.  
PR 06-JUL-1999: 99US-0142390.  
PR 08-JUL-1999: 99US-0142803.  
PR 09-JUL-1999: 99US-0142920.  
PR 12-JUL-1999: 99US-0142927.  
PR 13-JUL-1999: 99US-0143542.  
PR 14-JUL-1999: 99US-0143624.  
PR 15-JUL-1999: 99US-0144005.

```

PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148341.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 01-SEP-1999; 99US-0152363.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.

```

```

PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 22.0%; Score 58; DB 21; Length 67;
Best Local Similarity 39.0%; Pred. No. 15;
Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

OY 7 ERRKHLFVQDPQTCCKSKNTDSRCARQLELNERTC--RC 45
Db 7 eyrvellnklaqctfnkc--vdkrykeaelmgenscidrc 45

RESULT 14
AAG08909 standard; Protein; 67 AA.
ID AAG08909
XX
AC AAG08909;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 6630.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.

```

PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 28-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0132863.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143524.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151085.  
PR 27-AUG-1999; 99US-0151086.  
PR 27-AUG-1999; 99US-0151086.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.

PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 22.0%; Score 58; DB 21; Length 67;  
Best Local Similarity 39.0%; Pred. No. 15;  
Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

QY 7 ERKHLFVODPQTCKGCKNTDSCKAROLELNERTC--RC 45  
Db 7 eyrvellnklaqtcfknc--vdkrykeaelmngenscidrc 45

## RESULT 15

AAG43389  
ID AAG43389 standard; Protein: 67 AA.

XX AAG43389;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 54226.

KM Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;

KM termination sequence.

XX Arabidopsis thaliana.

PN EPI033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 16-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132464.  
PR 05-MAY-1999; 99US-0132465.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 17-JUN-1999; 99US-0139453.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139819.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144335.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.



**THIS PAGE BLANK (USPTO)**

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:20:19 ; Search time 21.83 Seconds  
(without alignments)  
301.523 Million cell updates/sec

Title: US-09-579-420-1

Sequence: 1 PCGPCSERKHLFVQDPQC.....NTDSRCKARQLELNERTCRC 45

Scoring table: BLOSUM62

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 92817

```
Minimum DB seq length: 0
```

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Database :

```

1:  SP TREM 17: *
2:  SP Archea: *
3:  SP Bacteria: *
4:  SP Fungi: *
5:  SP Human: *
6:  SP Invertebrate: *
7:  SP Mammal: *
8:  SP MHC: *
9:  SP Organelle: *
10: SP Phage: *
11: SP Plant: *
12: SP Rodent: *
13: SP Virus: *
14: SP Vertebrate: *
15: SP Unclassified: *

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59.5	22.5	77	5	Q23771	Q23771 chironomus
2	54.5	20.6	63	5	Q23803	Q23803 chironomus
3	54.5	20.6	72	12	Q75533	Q75533 human immun
4	53	20.1	43	5	O9VNM2	O9vnd2 drosophila
5	53	20.1	45	5	O9VNM2	O9vnm2 drosophila
6	52	19.7	81	10	O9AVE2	O9ave2 arabidopsis
7	51.5	19.5	83	5	Q23783	Q23783 chironomus
8	51	19.3	71	10	O9PRE0	Q91re0 brassica ca
9	49.5	18.8	72	12	O9EXG2	Q91ex2 human immun
10	49.5	18.8	87	2	O9A1S8	Q9a1s8 chlamydogli
11	48.5	18.4	98	9	O4B496	O4b496 bacteriophi
12	48.5	18.4	99	5	O9N329	O9n329 caenorhabdi
13	48	18.2	61	2	O9ZH19	O9zh19 desulfotoma
14	48	18.2	66	5	O9VE14	O9ve14 drosophila
15	48	18.2	81	10	O82789	O82789 brassica o
16	48	18.2	88	2	P94653	P94653 chlamydia p
17	47.5	18.0	60	6	O9TS92	O9ts92 bos taurus
18	47.5	18.0	62	2	O9X1L9	O9x1l9 thermotoga
19	47	17.8	42	6	O46620	O46620 equus asinu

20	47	17.8	59	5	P82107	hiirudo medii
21	47	17.8	84	13	Q90248	Q90248 bombyx mori
22	46.5	17.6	68	4	Q9UE57	Q9UE57 homo sapiens
22	46.5	17.6	72	12	Q75531	Q75531 human immun
23	46.5	17.6	72	12	Q75529	Q75529 human immun
24	46.5	17.6	72	12	Q75530	Q75530 human immun
25	46.5	17.6	72	12	Q75532	Q75532 human immun
26	46.5	17.6	72	12	Q75533	Q75533 human immun
27	46.5	17.6	72	12	Q75537	Q75537 human immun
28	46.5	17.6	72	12	Q75538	Q75538 human immun
29	46.5	17.6	95	5	Q23373	Q23373 chironomus
30	46	17.4	48	6	P79380	P79380 sus scrofa
31	46	17.4	68	6	Q9N139	Q9N139 bos taurus
32	46	17.4	70	2	Q34083	Q34083 streptococc
33	46	17.4	73	5	Q62554	Q62554 mytilus edu
34	46	17.4	76	11	Q70556	Q70556 mus musculus
35	46	17.4	98	12	Q9YR19	Q9YR19 human cytom
36	45.5	17.2	62	6	Q9TU15	Q9TU15 canis famill
37	45.5	17.2	86	10	Q9MG33	Q9MG33 arabidopsis
38	45.5	17.2	100	5	P90911	P90911 caenorhabdi
39	45	17.0	48	2	Q9RPF5	Q9RPF5 mycoplasma
40	45	17.0	72	5	Q9VZQ4	Q9VZQ4 drosophila
41	45	17.0	76	11	Q70557	Q70557 mus musculu
42	45	17.0	78	10	Q9S9H8	Q9S9H8 vigna unguicu
43	45	17.0	79	10	Q9MB54	Q9MB54 brassica oler
44	45	17.0	84	10	Q9XH47	Q9XH47 pinus taeda
45	45	17.0	89	12	Q69699	Q69699 human immun

## ALIGNMENTS

[illegible]

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;  
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.  
 OX NCBI\_TaxID=7153;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89255447; PubMed=2470756;  
 RA Dignam S.S., Yang L., Iezzi M., Case S.T.;  
 RT "Identification of a developmentally regulated gene for a 140-kDa  
 RT secretory protein in salivary glands of Chironomus tentans larvae."  
 RL J. Biol. Chem. 264:9444-9452(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90269600; PubMed=2189782;  
 RA Dignam S.S., Case S.T.;  
 RT "Baldian ring 3 in Chironomus tentans encodes a 185-kDa secretory  
 RT protein which is synthesized throughout the fourth larval instar."  
 RL Gene 88:133-140(1990).  
 DR EMBL: M24160; AAA28263.1; -.  
 FT NON\_TER 1 1  
 FT 63 63  
 SO SEQUENCE 63 AA; 6963 MW; 1CBBF8CA3486F5CE CRC64;

Query Match 20.6%; Score 54.5; DB 5; Length 63;  
 Best Local Similarity 34.6%; Pred. No. 2.6;  
 Matches 9; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 20 CKCSKNTDSRCKAROLELNEBTRC 45  
 DB 14 CICECTTPATCEGKOTWCE-ACQC 38

RESULT 3  
 075533 PRELIMINARY; PRT; 72 AA.  
 AC 075533;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=704A.  
 RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U57241; AAB17801.1; -.  
 DR InterPro: IPR001831; HIV\_Tat.  
 DR Pfam: PF00539; Tat; 1  
 DR PRINTS: PR00055; HIVTATDOMAIN.  
 KW Envelope protein.  
 FT NON\_TER 1 1  
 FT 72 72  
 SO SEQUENCE 72 AA; 8333 MW; 6877B110FB082120 CRC64;

Query Match 20.6%; Score 54.5; DB 12; Length 72;  
 Best Local Similarity 41.2%; Pred. No. 2.9;  
 Matches 14; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

OY 1 PCGPCSERKHLFVODPQC-KSCSKNTDSRCA 33  
 DB 3 PVDPRLEPRKHPGSOPTACTKCYCKKCPHCA 36

RESULT 4  
 09VDN2 PRELIMINARY; PRT; 43 AA.  
 AC 09VDN2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CG5097 PROTEIN.  
 GN CG5097.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003730; AAF55758.1; -.  
 DR FlyBase: FBgn0038790; CG5097.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000966; Melittin-like.  
 DR Pfam: PF02067; Melittin-like.  
 DR PRINTS: PR00872; MTDIPTERA.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1  
 SO SEQUENCE 43 AA; 4597 MW; E54E722B14EB9DFE CRC64;

Query Match 20.1%; Score 53; DB 5; Length 43;  
 Best Local Similarity 52.6%; Pred. No. 3.1;  
 Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 18 QTCCKSCKN--TDSRCKAR 34  
 DB 25 QDCKCVCCKNGPKDCKCKSK 43

RESULT 5  
 09VM82



```

ID 09VM82 PRELIMINARY: PRT: 45 AA.
AC 09VM82;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG18461 PROTEIN.
GN CG17376 OR CG18461.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Dayenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan M., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AF003615; AAF52441.1; -;
DR Flybase; FBgn0042189; CG17376.
SQ SEQUENCE 45 AA; 4869 MW; F8F92B3B3FB88254 CRC64;

```

```

Query Match 20.1%; Score 53; DB 5; Length 45;
Best Local Similarity 33.3%; Pred. No. 3.2;
Matches 12; Conservative 4; Mismatches 14; Indels 6; Gaps 1;

```

```

OY 2 CGPSERRKHLFVODP-----OTCKCKNTDSRC 31
   ||| |::| |::| |::| |::| |::| |::| |::|
DB 8 CGPSPCRRLVKNKDNAPCWCAPCAKHACYNTTPKC 43

```

```

RESULT 6
O9AVE2 PRELIMINARY: PRT: 81 AA.
ID O9AVE2;
AC O9AVE2;
DT 01-JUN-2001 (Tremblrel. 17, Created)

```

```

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SCRB.
GN SCRB.
OS Arabidopsis lyrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=59689;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21149876; PubMed=11251101;
RA Kusaba M., Dwyer K., Hendershot J., Vrebalov J., Nasrallah J.B.,
RA Nasrallah M.E.;
RT "Self-incompatibility in the Genus Arabidopsis: Characterization of
RT the S locus in the outcrossing A. lyrata and its Autogamous Relative
RT A. thaliana.";
RL Plant Cell 13:627-643(2001).
DR EMBL; AB052754; BAB40985.1; -;
SQ SEQUENCE 81 AA; 9457 MW; 6AAE5C7FB24D291C CRC64;

```

```

Query Match 19.7%; Score 52; DB 10; Length 81;
Best Local Similarity 31.2%; Pred. No. 7;
Matches 15; Conservative 3; Mismatches 20; Indels 10; Gaps 2;

```

```

OY 1 PCGPSERRKHLFVODPOTCKSCSKN---TDSCKAROLEINERTC 45
   ||| |::| |::| |::| |::| |::| |::|
DB 38 PTPGCGNNGE-----ETCKKDEKNITRPPICQCKDKXDFARLDC 78

```

```

RESULT 7
ID 023783 PRELIMINARY: PRT: 83 AA.
AC 023783;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE BALBIANI RING C REPEAT UNIT (FRAGMENT).
OS Chironomus thummi thummi (Midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OX NCBI_Taxid=7155;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84236027; PubMed=7188354;
RA Baumelein H., Wobus U., Gerbi S., Kafatos F.C.;
RT "Characterization of a 249-bp tandemly repetitive, satellite-like
RT repeat in the translated portion of Balbiani ring c of Chironomus
RT thummi.";
RL EMBL J. 1:641-647(1982).
DR EMBL; X01859; CAA25979.1; -;
FT NON_TER 1 83
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 8772 MW; 5EE3B8B0B9D04F6 CRC64;

```

```

Query Match 19.5%; Score 51.5; DB 5; Length 83;
Best Local Similarity 22.7%; Pred. No. 8.3;
Matches 10; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

```

```

OY 3 GCPSERRKHLFVODPOTCKCKNTDS-ROKAROLEINERTC 45
   ||| |::| |::| |::| |::| |::| |::|
DB 32 GPKTSKSGKPKPKPEKGSAMKRTLEKCAKKNGRNSKRC 75

```

```

RESULT 8
O9LREO PRELIMINARY: PRT: 71 AA.
ID O9LREO;
AC O9LREO;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

```

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE S LOCUS PROTEIN 11-32 (FRAGMENT).  
 GN SP11-32.  
 OS Brassica campestris (Field mustard).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;  
 OC eurosids II: Brassicales: Brassicaceae: Brassica.  
 NC NCBI\_TaxID=3711;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S32(50-11T);  
 RX MEDLINE=20273842; PubMed=10812061;  
 RA Motanabe M., Ito A., Takada Y., Ninomiya C., Kakizaki T., Takahata Y.,  
 RA Hatakeyama K., Hinata K., Suzuki G., Takasaki T., Satia Y., Shiba H.,  
 RA Takayama S., Isogai A.;  
 RT "Highly divergent sequences of the pollen self-incompatibility (S)  
 RT gene in class-I S haplotypes of Brassica campestris (syn. rapa) L.";  
 RL FEBS Lett. 473:139-144(2000).  
 DR EMBL: AB039756; BAA96394.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 71 AA; 7928 MW; 1E8E5E88D8720F97 CRC64;

Query Match 19.3%; Score 51; DB 10; Length 71;  
 Best Local Similarity 29.0%; Pred. No. 8.6;  
 Matches 9; Conservative 5; Mismatches 7; Indels 10; Gaps 1;

OY 15 ODPOTCKSCKNTDSCKARQLEINERTC 45  
 DB 47 KDPALCSCICRHHGCR-----RCPCC 67

RESULT 9  
 O98XG2  
 ID O98XG2 PRELIMINARY; PRT; 72 AA.  
 AC O98XG2;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE TAT PROTEIN (FRAGMENT).  
 GN TAT.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses: Retroviridae: Lentivirus.  
 NC NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PAIR C MOTHER;  
 RA Hsain M., Hahn T., Jedavalli V.R.K., Ahmad N.;  
 RT "Molecular Characterization of HIV Type 1 tat Gene from Mother-Infant  
 RT Isolates Associated with Perinatal Transmission.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY07033; AAG32897.1; -;  
 FT NON\_TER 72  
 SQ SEQUENCE 72 AA; 8225 MW; B716DB42042D5D46 CRC64;

Query Match 18.8%; Score 49.5; DB 12; Length 72;  
 Best Local Similarity 39.4%; Pred. No. 14;  
 Matches 13; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

OY 1 PCGPCSERRKHLFYODPOTC-KCSCKNTDSRCK 32  
 DB 3 PVPRLPRKRKHPGSPKTKACSKCYKACMHCQ 35

RESULT 10  
 O9A1S8  
 ID O9A1S8 PRELIMINARY; PRT; 87 AA.  
 AC O9A1S8;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE SMALL CYSTEINE-RICH OUTER MEMBRANE LIPOPROTEIN.

GN OMLA.  
 OS Chlamydia abortus.  
 OC Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia.  
 NC NCBI\_TaxID=83555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EBA;  
 RX MEDLINE=21078680; PubMed=11211261;  
 RA Bush R.M., Everett K.D.;  
 RT "Molecular evolution of the Chlamydiaceae.";  
 RL Int. J. Syst. Evol. Microbiol. 51:203-220(2001).  
 DR EMBL: AF240773; AAG60549.1; -;  
 KW Lipoprotein.  
 SQ SEQUENCE 87 AA; 8972 MW; F6DB1E88DAF57D80 CRC64;

Query Match 18.8%; Score 49.5; DB 2; Length 87;  
 Best Local Similarity 24.5%; Pred. No. 16;  
 Matches 13; Conservative 4; Mismatches 13; Indels 23; Gaps 2;

OY 1 PCGPCSERRKHLFYODPOTCKSCKNTDSRCK 32  
 DB 36 PCNCGKKKDKGCSPCCTTPSCITPCGSECNSSVGPOA--KCTSLDGRCK 86

RESULT 11  
 O48496  
 ID O48496 PRELIMINARY; PRT; 98 AA.  
 AC O48496;  
 DT 01-JUN-1998 (TReMBLrel. 06, Created)  
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)  
 DE COMPLETE NUCLEOTIDE SEQUENCE.  
 OS Bacteriophage SP1.  
 OC Viruses: dsDNA viruses, no RNA stage: Tailed phages: Siphoviridae.  
 NC Lambda phage group.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Alonso J.C., Luder G., Stiege A.C., Chai S., Weise F., Trautner T.A.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X97918; CAA6503.1; -;  
 SQ SEQUENCE 98 AA; 10724 MW; EC648DF58CAF7BEFF CRC64;

Query Match 18.4%; Score 48.5; DB 9; Length 98;  
 Best Local Similarity 34.1%; Pred. No. 24;  
 Matches 15; Conservative 3; Mismatches 23; Indels 3; Gaps 1;

OY 2 CGPCSEERRKHLFYODPOTCKSCKNTDSCKARQLEINERTC 45  
 DB 11 CGPVPSKKKSINKVEHR---ACKLDSDIVKPMSPRLNERVGR 51

RESULT 12  
 O9N329  
 ID O9N329 PRELIMINARY; PRT; 99 AA.  
 AC O9N329;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE HYPOTHETICAL PROTEIN Y59E9AL.5.  
 GN Y59E9AL.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota: Metazoa: Nematoda: Chromadorea: Rhabditida: Rhabditidae;  
 OC Rhabditidae: Peloderinae: Caenorhabditis.  
 NC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for

```

RT Investigating biology "The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024838; AAF60819.1; -.
SQ SEQUENCE 99 AA; 11325 MW; EB3CCC5BFB7DAECC CRC64;

Query Match 18.4%; Score 48.5; DB 5; Length 99;
Best Local Similarity 37.8%; Pred. No. 25;
Matches 14; Conservative 3; Mismatches 13; Indels 7; Gaps 2;

QY 2 CGPSEERRK-----HLFVDP-QTCCKSCKNFTDRC 31
| | | | | | | | | | | | | | | | | | | |
Db: 51 CCACMMRRKKESTTKVCVDDCTCTCSASRCSRC 87

RESULT 13
ID Q9ZHI9 PRELIMINARY; PRT; 61 AA.
AC Q9ZHI9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FERRDOXIN.
GN FDY.
OS Desulfotomaculum thermocisternum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Desulfotomaculum.
OX NCBI_TaxID=42471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ST90;
RA Larsen O., Lien T., Birkeland N.-K.;
RT "Disimilatory sulfite reductase from Archaeoglobus profundus and
RT Desulfotomaculum thermocisternum: phylogenetic and structural
RT implications from gene sequences.";
RL Extremophiles 0:0-0(1999).
DR EMBL; AF074396; AAC96106.1; -.
DR HSSP; P46797; 1R0F.
DR InterPro; IPR001080; 3FE4S_ferrixdn.
DR InterPro; IPR001450; 4FE4S_ferrixdn.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00352; 3FE4SFDOXIN.
DR PROSITE; PS00196; 4FE4S_FERRDOXIN; 2.
KW Iron-sulfur.
SQ SEQUENCE 61 AA; 6408 MW; EIDF4EAF95CAAC CRC64;

Query Match 18.2%; Score 48; DB 2; Length 61;
Best Local Similarity 26.5%; Pred. No. 19;
Matches 13; Conservative 7; Mismatches 19; Indels 10; Gaps 2;

QY 2 CGPSE-----RRKHLFVDPQTCCKSCKNFTDRCAROLELNER 41
| | | | | | | | | | | | | | | | | | | |
Db: 14 CGECADSCPSVLEMKGKAFVANPDC-LGCETCVSCPSGAVTLER 61

RESULT 14
ID Q9VEI4 PRELIMINARY; PRT; 66 AA.
AC Q9VEI4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG7606 PROTEIN.
GN CG7606.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

```

```

OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaniatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Bailley R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003718; AAF5437.1; -.
DR FlyBase; FBgn0040565; CG7606.
SQ SEQUENCE 66 AA; 6812 MW; 8151AP9B3BFB5FC CRC64;

Query Match 18.2%; Score 48; DB 5; Length 66;
Best Local Similarity 28.1%; Pred. No. 21;
Matches 9; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 14 VQDPQTCCKSCKNFTDRCAROLELNERTCRC 45
| | | | | | | | | | | | | | | | | | | |
Db: 22 VEEPEOVECGCGCGPC---LSCGSRSCGC 49

RESULT 15
ID O82789 PRELIMINARY; PRT; 81 AA.
AC O82789;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE POLLEN COAT PROTEIN CLASS 'A', NO. 1 PRECURSOR (FRAGMENT).
GN PCP-A1.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:20:39 ; Search time 10.04 Seconds

(without alignments)  
164.334 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264  
Sequence: 1 PCGPCSERRKHLEFVDPQTC.....NTDSRCKAROLELNERTCRC 45

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 11805

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	22.0	83	1	IM10_ARATH
2	54	20.5	73	1	MT_DREPO
3	54	20.5	74	1	MT1_CABEL
4	53.5	20.3	62	1	MT2_CABEL
5	53	20.1	62	1	MT_XENLA
6	53	20.1	63	1	MT_CHICK
7	53	20.1	66	1	MT3_RAT
8	53	20.1	68	1	MT3_MOUSE
9	52.5	19.9	68	1	CRS5_YEAST
10	52	19.7	63	1	MT2_COLLI
11	52	19.7	68	1	MT3_HUMAN
12	51.5	19.5	58	1	MT1_SCYSE
13	51.5	19.5	67	1	IBB1_DIOGL
14	51	19.3	68	1	MT3_BOVIN
15	51	19.3	68	1	MT3_HORSE
16	51	19.3	68	1	MT3_PIG
17	51	19.3	74	1	MT_CRAVI
18	51	19.3	91	1	ACCD_ANTFO
19	49.5	18.8	59	1	MT1_CAUST
20	49	18.6	35	1	SCXP_ANDMA
21	49	18.6	96	1	HMVA_MERJA
22	48.5	18.4	58	1	MT_POTPO
23	48.5	18.4	87	1	OM3_CHIPS
24	48	18.2	58	1	MT2_CALSI
25	47.5	18.0	62	1	MT4_HUMAN
26	47.5	18.0	71	1	MT21_MYTED
27	47.5	18.0	82	1	IBB1_PHANAN
28	47	17.8	57	1	MT2_SCYSE
29	47	17.8	60	1	MTA_THERC
30	46.5	17.6	58	1	MT_ASTRU
31	46	17.4	51	1	MT2_CANCA
32	46	17.4	58	1	MT_CARMA
33	46	17.4	60	1	MT_CYPCA

34	46	17.4	72	1	MT11_MYTED	P80246 mytilus edu
35	46	17.4	85	1	EC2_ARATH	Q42377 arabidopsis
36	45.5	17.2	36	1	SCK3_LEIOH	P45660 leirus qui
37	45.5	17.2	58	1	MT1_HOMAM	P29499 homarus ame
38	45.5	17.2	60	1	MT_AMEME	O42152 ambystoma m
39	45.5	17.2	61	1	MT_C_YEAST	P07215 saccharomyc
40	45.5	17.2	62	1	NEU2_HORSE	P01182 equus cabal
41	44.5	16.9	92	1	MT4_MOUSE	P47945 mus musculi
42	44.5	16.9	63	1	IBB_VICPA	P24661 vicia faba
43	44.5	16.9	91	1	HRK_HUMAN	O00198 homo sapien
44	44	16.7	49	1	HSP1_PTC	P04101 sus scrofa
45	44	16.7	64	1	MTCO_HELPO	P55947 helix pomat

## ALIGNMENTS

RESULT	1	STANDARD	PT	83 AA.
IM10_ARATH				
AC	O92W33			
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DE	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10.			
GN	TIM10 OR AT2G29530 OR F16P2.9.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:			
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:			
OC	eurosid II: Brassicales: Brassicaceae: Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bauer M.F., Brunner M., Hofmann S.:			
RT	"Cloning and mapping of the Tim10/DDP gene family encoding small zinc			
RT	finger proteins involved in mitochondrial carrier import."			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. COLUMBIA:			
RA	MEDLINE=20083487; PubMed=10617197;			
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,			
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,			
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,			
RA	Moffat K.S., Cronin L.A., Shen M., Vankken S.E., Umayam L.,			
RA	Talton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,			
RA	Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,			
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,			
RT	Verter J.C.;			
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis			
RT	thaliana."			
RL	Nature 402:761-768(1999).			

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AF150093; AAD39999.1; -  
KW TRANSPORT; Protein transport; Translocation; Mitochondrion;  
KW Inner membrane.  
SQ SEQUENCE 83 AA: 9339 MW: 135519B3FEEF331 CRC64;

Query Match 22.0% Score 58; DB 1; Length 83;  
Best Local Similarity 39.0% Pred. No. 1.6; Indels 4; Gaps 2;  
Matches 16; Conservative 4; Mismatches 17;  
7 ERRKHLFVDPQTCSCSKNTDSRCKAROLELNERTC--RC 45

Db 23 EYRVELFNKLAOTCFNKCC--VDKRYKEAEELMGENSCIDRC 61

## RESULT 2

MT\_DREPO STANDARD: PRT: 73 AA.

AC 094550;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE METALLOTHIONEIN.

OS Dreissena polymorpha (Zebra mussel).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heterococoncha; Veneroida;

OC Dreissenoida; Dreissenidae; Dreissena.

NCBI\_TaxId=45954;

ON [1]

RP SEQUENCE FROM N.A.

RA Sezekan S.R., Engelken J., Hildebrandt A.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 2-40.

RA Sezekan S.R., Engelken J., Hildebrandt A.;

RL Submitted (JUL-1997) to the SWISS-PROT data bank.

CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR SEQUESTRATION OF TOXIC METAL IONS (BY SIMILARITY).

CC -1- INDUCTION: BY CADMIUM.

CC -1- SIMILARITY: BELONGS TO FAMILY 2 IN METALLOTHIONEIN SUPERFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: U67347; AAB07548.1; -

DR HSSP: P02795; 2MHU.

DR InterPro: IPR001008; Metallthion\_mollusc.

DR PRINTS: PR00875; MTMOLLUSC.

KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.

SQ SEQUENCE 73 AA: 7364 MW: DD3398705C4DAEE9 CRC64;

Query Match 20.5%; Score 54; DB 1; Length 73;

Best Local Similarity 31.1%; Pred. No. 4.3; 11; Indels 16; Gaps 3;

Matches 14; Conservative 4; Mismatches 11; Indels 16; Gaps 3;

OY 3 GPCSERRKHLFVDPQTKC--SCKNTDSRCAROLELNERTCRC 45

Db 18 GSCS-----DCSNCKGSGCKSPKPCGCKNV-----TCNC 48

## RESULT 3

MT1\_CAEEL

ID MT1\_CAEEL STANDARD: PRT: 74 AA.

AC P17511;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE METALLOTHIONEIN-1 (MT-1).

GN MT1-1 OR MET-1 OR K11G9.6.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

ON NCBI\_TaxId=6239;

RP SEQUENCE FROM N.A.

RX MEDLINE=90094407; Pubmed=2294106;

RA Slice L.W., Freedman J.H., Rubin C.S.;

RT "Purification, characterization, and cDNA cloning of a novel metallothionein-like, cadmium-binding protein from Caenorhabditis

RT elegans.";

RL J. Biol. Chem. 265:256-263(1990).

RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.

RC STRAIN-BRISTOL N2;

RX MEDLINE=90262552; Pubmed=2344361;

RA Imagawa M., Onozawa T., Okumura K., Osada S., Nishihara T., Kondo M.;

RT "Characterization of metallothionein cDNAs induced by cadmium in the

RT nematode Caenorhabditis elegans.";

RL Biochem. J. 268:237-240(1990).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=93155063; Pubmed=8428932;

RA Freedman J.H., Slice L.W., Dixon D., Fire A., Rubin C.S.;

RT "The novel metallothionein genes of Caenorhabditis elegans.

RT structural organization and inducible, cell-specific expression.";

RL J. Biol. Chem. 268:2554-2564(1993).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE=95151184; Pubmed=7848551;

RA Kugawa F., Yamamoto H., Osada S., Aoki M., Imagawa M., Nishihara T.;

RT Metallothionein genes in the nematode Caenorhabditis elegans and

RL Biomed. Environ. Sci. 7:222-231(1994).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA Greco T., Bradshaw H.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION

CC ELEMENTS.

CC -1- INDUCTION: BY CADMIUM.

CC -1- DOMAIN: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE

CC ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER

CC METALLOTHIONEINS.

CC -1- SIMILARITY: BELONGS TO FAMILY 6 IN METALLOTHIONEIN SUPERFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL: M92909; AAA28110.1; -

DR EMBL: X53244; CAA37334.1; -

DR EMBL: D17364; BAA04180.1; -

DR EMBL: U64853; AAB04979.1; -

DR PIR: S09714; S09714.

DR PIR: B45206; B45206.

DR HSSP: P04355; 4MT2.

DR WormPep: K11G9.6; CE07379.

DR InterPro: IPR000853; Metallthion\_nemat.

DR PRINTS: PR00876; MTNEMATODE.

KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.

FT INIT MET

FT CONFLICT

FT SEQUENCE

OY 20 CKSCCKNTDSRCAROLELNERTCRC 45

Db 2 CKCKCKKCKCKGCKGCK-----CEC 19

## RESULT 4

MT2\_CAEEL

Query Match 20.5%; Score 54; DB 1; Length 74;

Best Local Similarity 34.6%; Pred. No. 4.4;

Matches 9; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

ID WT2.CAEEL STANDARD: PRT: 62 AA.  
 AC p17512;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE).  
 GN MT-2 OR MET-2 OR T08G5.10.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90094407; PubMed=2294106;  
 RA Slice L.W., Freedman J.H., Rubin C.S.;  
 RT "Purification, characterization, and cDNA cloning of a novel  
 RT metallothionein-like, cadmium-binding protein from Caenorhabditis  
 RT elegans.";  
 RL J. Biol. Chem. 265:256-263(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-14.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=90262552; PubMed=2344361;  
 RA Imagawa M., Onozawa T., Okumura K., Osada S., Nishihara T., Kondo M.;  
 RT "Characterization of metallothionein cDNAs induced by cadmium in the  
 RT nematode Caenorhabditis elegans.";  
 RL Biochem. J. 268:237-240(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93155063; PubMed=8428932;  
 RA Freedman J.H., Slice L.W., Dixon D., Fire A., Rubin C.S.;  
 RT "The novel metallothionein genes of Caenorhabditis elegans.  
 RT Structural organization and inducible, cell-specific expression.";  
 RL J. Biol. Chem. 268:2554-2564(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=95151184; PubMed=7848551;  
 RA Kugawa F., Yamamoto H., Osada S., Aoki M., Imagawa M., Nishihara T.;  
 RT "Metallothionein genes in the nematode Caenorhabditis elegans and  
 RT metal inducibility in mammalian culture cells.";  
 RL Biomed. Environ. Sci. 7:222-231(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Slave R.;  
 RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION  
 CC ELEMENTS.  
 CC -1- INDUCTION: BY CADMIUM.  
 CC -1- DOMAIN: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE  
 CC ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER  
 CC METALLOTHIONEINS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 6 IN METALLOTHIONEIN SUPERFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M92910: AAA28111.1: -  
 CC EMBL: M32386: AAA28117.1: -  
 CC EMBL: M32387: AAA28118.1: -  
 CC EMBL: X53245: CAA37335.1: -  
 CC EMBL: D17365: BAA04181.1: -  
 CC EMBL: Z81589: CAB61028.1: -  
 CC PIR: A34905: A34905.  
 CC PIR: S09715: S09715.  
 CC PIR: A45206: A45206.  
 CC HSSP: P04355: 4MT2.

DR NormBep: T08G5.10: CE25109.  
 DR InterPro: IPR000853; Mtlthion\_nemat.  
 DR PRINTS: PR00876; MTNEMATODE.  
 KW Metal-binding; Metal-chiolate cluster; Chelation; Cadmium.  
 FT INT MET 0 0  
 SQ SEQUENCE 62 AA; 6462 MW; 5D33797A1CDBD797 CRC64;  
 Query Match 20.3%; Score 53.5; DB 1; Length 62;  
 Best Local Similarity 34.6%; Pred. No. 4.3;  
 Matches 9; Conservative 2; Mismatches 10; Indels 5; Gaps 1;  
 Oy 20 CKCCKNTDSCRKARQELNERTCRC 45  
 Db 2 CKCCKNQCNCNT-----GTRKDCD 22  
 RESULT 5  
 MT\_XENIA STANDARD: PRT: 62 AA.  
 ID MT\_XENIA  
 AC 005890;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE METALLOTHIONEIN.  
 GN MT-A.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Liver;  
 RX MEDLINE=93263990; PubMed=8494609;  
 RA St Jacques E., Seguin C.;  
 RT "Cloning and nucleotide sequence of a complementary DNA encoding  
 RT heavy metals.";  
 RL DNA Cell Biol. 12:329-340(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93263991; PubMed=8494610;  
 RA Muller J.-P., Wouters-Tyrou D., Errais N.-E., Vedel M., Touzet N.,  
 RA Mesnard J., Sautiere P., Wegnez M.;  
 RT "Molecular cloning and expression of a metallothionein mRNA in  
 RT Xenopus laevis.";  
 RL DNA Cell Biol. 12:341-349(1993).  
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS.  
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:  
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA  
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11  
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE  
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U16449: AAB50616.1: -  
 CC EMBL: M96729: AAB5949.1: -  
 CC EMBL: X69380: CAA49177.1: -  
 CC HSSP: P04355; IMRT.  
 CC InterPro: IPR003019; Metallothion.  
 CC InterPro: IPR000066; Mtlthion\_vert.  
 CC Pfam: PF00131; metalthio.1.  
 CC PRINTS: PR00860; MTVERTEBRATE.

DR PROSITE: PS00203; METALLOTHIONEIN\_VRT; 1.  
 KW Metal-binding; Metal-Chiolate cluster; Chelation; Acetylation.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT DOMAIN 31 30 BETA.  
 FT METAL 6 6 ALPHA.  
 FT METAL 8 8 CLUSTER B.  
 FT METAL 14 14 CLUSTER B.  
 FT METAL 16 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER B.  
 FT METAL 22 22 CLUSTER B.  
 FT METAL 25 25 CLUSTER B.  
 FT METAL 27 27 CLUSTER B.  
 FT METAL 30 30 CLUSTER B.  
 FT METAL 34 34 CLUSTER A.  
 FT METAL 35 35 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT METAL 38 38 CLUSTER A.  
 FT METAL 42 42 CLUSTER A.  
 FT METAL 45 45 CLUSTER A.  
 FT METAL 49 49 CLUSTER A.  
 FT METAL 51 51 CLUSTER A.  
 FT METAL 58 58 CLUSTER A.  
 FT METAL 60 60 CLUSTER A.  
 FT METAL 61 61 CLUSTER A.  
 SQ SEQUENCE 62 AA; 6403 MW; AF7329487A3C7982 CRC64;

Query Match 20.18; Score 53; DB 1; Length 62;  
 Best Local Similarity 33.38; Pred. No. 4.9;  
 Matches 12; Conservative 2; Mismatches 16; Gaps 1;

OY 16 DPORCK-----CSCKNYDNRKAROLELNRRRCRC 45  
 Db 2 DPORCKCETGASCSCGTTTSCSNCKTSCCKKSCSC 37

RESULT 6  
 MT\_CHICK  
 ID MT\_CHICK STANDARD; PRT; 63 AA.  
 AC P09576;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE METALLOTHIONEIN (MT).  
 OS Gallus gallus (Chicken), Melagris gallopavo (Common turkey),  
 OS Phasianus colchicus colchicus (Ring-necked pheasant),  
 OS Anas platyrhynchos (Domestic duck), and  
 OS Cairina moschata (Muscovy duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 9103, 9057, 8839, 8855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Chicken; STRAIN=WHITE LEGHORN;  
 RX MEDLINE=88124253; PubMed=3340548;  
 RA Wei D., Andrews G.K.;  
 RT "Molecular cloning of chicken metallothionein. Deduction of the  
 complete amino acid sequence and analysis of expression using cloned  
 cDNA.";  
 RL Nucleic Acids Res. 16:537-553(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Chicken;  
 RX MEDLINE=90034180; PubMed=2806910;  
 RA Fernando L.P., Andrews G.K.;  
 RT "Cloning and expression of an avian metallothionein-encoding gene.";  
 RL Gene 81:177-183(1989).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=Chicken; TISSUE=Liver;  
 RX MEDLINE=88124831; PubMed=2448773;

RA McCormick C.C., Fullmer C.S., Garvey J.S.;  
 RT "Amino acid sequence and comparative antigenicity of chicken  
 metallothionein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:309-313(1988).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=Chicken;  
 RX MEDLINE=89141100; PubMed=2645390;  
 RA Fernando L.P., Wei D., Andrews G.K.;  
 RT "Structure and expression of chicken metallothionein.";  
 RL J. Nutr. 119:309-318(1989).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=A.platyrhynchos, and C.moschata; TISSUE=Liver;  
 RA Lin L.-Y., Lee Y.J.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE.  
 RC SPECIES=A.platyrhynchos, and C.moschata;  
 RX MEDLINE=90226357; PubMed=2327997;  
 RA Lin L.-Y., Huang P.C.;  
 RT "Complete homology in metallothionein from two genera of ducks and  
 their hybrids.";  
 RL Biochem. Biophys. Res. Commun. 168:182-187(1990).  
 RN [7]  
 RP SEQUENCE.  
 RC SPECIES=Mule duck [Common duck X Muscovy duck];  
 RX MEDLINE=91027866; PubMed=2223844;  
 RA Lin L.-Y., Liu L.-F., Tam M.F., Huang P.C., Vestling M., Fenselau C.;  
 RT "Primary sequence of duck metallothionein.";  
 RL Biochim. Biophys. Acta 1041:31-35(1990).  
 RN [8]  
 RP SEQUENCE OF 15-57 FROM N.A.  
 RC SPECIES=W.gallopavo, and P.colchicus; TISSUE=Liver;  
 RX MEDLINE=93247065; PubMed=8483164;  
 RA Shartzer K.L., Kage K., Sobieski R.J., Andrews G.K.;  
 RT "Evolution of avian metallothionein: DNA sequence analyses of the  
 turkey metallothionein gene and metallothionein cDNAs from pheasant  
 and quail.";  
 RL J. Mol. Evol. 36:255-262(1993).  
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 RESIDUES THAT BIND VARIOUS HEAVY METALS.  
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:  
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA  
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11  
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE  
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.  
 CC  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X06749; CAA29924.1; -  
 CC EMBL: X62514; CAA44372.1; -  
 CC EMBL: X62510; CAA44369.1; -  
 CC EMBL: U34231; AAC60048.1; -  
 CC EMBL: U34230; AAC60047.1; -  
 CC PIR: A28113; A28113.  
 CC PIR: J00030; J00030.  
 CC PIR: S01750; S01750.  
 CC PIR: S13154; S13154.  
 CC PIR: A34620; A34620.  
 CC PIR: A34958; A34958.  
 CC PIR: B34620; B34620.  
 CC PIR: C34620; C34620.  
 CC PIR: S18180; S18180.  
 CC PIR: S18182; S18182.  
 CC PIR: S33381; S33381.



DR HSSP: P02795; 2MHU.  
 DR InterPro: IPR003019; Metallothion.  
 DR InterPro: IPR000006; Metallothion\_vert.  
 DR Pfam: PF00131; metalthio: 1.  
 DR PRINTS: PR00860; MTVERTERRATE.  
 DR PROSITE: PS00203; METALLOTHIONEIN\_VRT: 1.  
 KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc.  
 FT DOMAIN 1 30  
 FT METAL 31 63 ALPHA.  
 FT METAL 6 6 CLUSTER B.  
 FT METAL 8 8 CLUSTER B.  
 FT METAL 14 14 CLUSTER B.  
 FT METAL 16 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER B.  
 FT METAL 22 22 CLUSTER B.  
 FT METAL 25 25 CLUSTER B.  
 FT METAL 27 27 CLUSTER B.  
 FT METAL 30 30 CLUSTER B.  
 FT METAL 34 34 CLUSTER A.  
 FT METAL 35 35 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT METAL 38 38 CLUSTER A.  
 FT METAL 42 42 CLUSTER A.  
 FT METAL 45 45 CLUSTER A.  
 FT METAL 49 49 CLUSTER A.  
 FT METAL 51 51 CLUSTER A.  
 FT METAL 59 59 CLUSTER A.  
 FT METAL 61 61 CLUSTER A.  
 FT METAL 62 62 CLUSTER A.  
 SQ SEQUENCE 63 AA; 6461 MW; 0062422501B9CC84 CRC64;

Query Match 20.1%; Score 53; DB 1; Length 63;  
 Best Local Similarity 30.0%; Pred. No. 4.9;  
 Matches 12; Conservative 4; Mismatches 10; Indels 14; Gaps 2;

OY 16 DPOTCKC-----SKNDSRCKAROLEINERTCRC 45  
 DB 2 DPQDCTCAAGDSCSCAGSCCKNCRCRS---CRKSCCSC 37

RESULT 7  
 ID MT3\_RAT STANDARD; PRT; 66 AA.  
 AC P37361;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).  
 GN MT3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94018480; PubMed=8412560;  
 RA Kobayashi H., Uchida Y., Ihara Y., Nakajima K., Kohsaka S.,  
 RA Miyatake T., Tsuji S.;  
 RT "Molecular cloning of rat growth inhibitory factor cDNA and the  
 RT expression in the central nervous system."  
 RL Brain Res. Mol. Brain Res. 19:188-194(1993).  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Glial tumor;  
 RA Amoureux M.C., Rehsaus E., Wurch T., Colpaert F.C., Pauwels P.J.;  
 RN Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 RN 13  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Chapman G.A., Kille P.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS ZINC AND COPPER ATOMS AND

CC ONLY A NEGLIGIBLE AMOUNT OF CADMIUM (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: BRAIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: S65838; AAB28366.1; -  
 CC EMBL: X89603; CAA61762.1; -  
 CC EMBL: Y08235; CAA69404.1; -  
 CC DR HSSP: P18055; IMRB.  
 DR InterPro: IPR003019; Metallothion.  
 DR InterPro: IPR000006; Metallothion\_vert.  
 DR Pfam: PF00131; metalthio: 1.  
 DR PRINTS: PR00860; MTVERTERRATE.  
 DR PROSITE: PS00203; METALLOTHIONEIN\_VRT: 1.  
 KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;  
 KW Acetylation.  
 FT MOD\_RES 1 1  
 FT DOMAIN 1 30  
 FT METAL 31 66 ALPHA.  
 FT METAL 6 6 CLUSTER B (BY SIMILARITY).  
 FT METAL 8 8 CLUSTER B (BY SIMILARITY).  
 FT METAL 14 14 CLUSTER B (BY SIMILARITY).  
 FT METAL 16 16 CLUSTER B (BY SIMILARITY).  
 FT METAL 20 20 CLUSTER B (BY SIMILARITY).  
 FT METAL 22 22 CLUSTER B (BY SIMILARITY).  
 FT METAL 25 25 CLUSTER B (BY SIMILARITY).  
 FT METAL 27 27 CLUSTER B (BY SIMILARITY).  
 FT METAL 30 30 CLUSTER B (BY SIMILARITY).  
 FT METAL 34 34 CLUSTER A (BY SIMILARITY).  
 FT METAL 35 35 CLUSTER A (BY SIMILARITY).  
 FT METAL 37 37 CLUSTER A (BY SIMILARITY).  
 FT METAL 38 38 CLUSTER A (BY SIMILARITY).  
 FT METAL 42 42 CLUSTER A (BY SIMILARITY).  
 FT METAL 45 45 CLUSTER A (BY SIMILARITY).  
 FT METAL 49 49 CLUSTER A (BY SIMILARITY).  
 FT METAL 51 51 CLUSTER A (BY SIMILARITY).  
 FT METAL 62 62 CLUSTER A (BY SIMILARITY).  
 FT METAL 64 64 CLUSTER A (BY SIMILARITY).  
 FT METAL 65 65 CLUSTER A (BY SIMILARITY).  
 SQ SEQUENCE 66 AA; 6809 MW; BE7538E85664EBF8 CRC64;

Query Match 20.1%; Score 53; DB 1; Length 66;  
 Best Local Similarity 35.3%; Pred. No. 5.2;  
 Matches 12; Conservative 5; Mismatches 5; Indels 12; Gaps 3;

OY 16 DPOTCKC-----SKNDSRCKAROLEINERTCRC 45  
 DB 2 DPETCPCTGSGCTCSD-KCKC-----KGCKC 27

RESULT 8  
 ID MT3\_MOUSE STANDARD; PRT; 68 AA.  
 AC P28184;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 11  
 RP SEQUENCE FROM N.A.

```

RC TISSUE=Brain;
RA MEDLINE=92335292; PubMed=1631128;
RX Palmer R.D., Findley S.D., Whitmore T.E., Duram D.M.;
"MT-II, a brain-specific member of the metallothionein gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6333-6337(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94314230; PubMed=8039715;
RA Naruse S., Igarashi S., Furuya T., Kobayashi H., Miyake T.,
  Tsuji S.;
RT "Structures of the human and mouse growth inhibitory factor-encoding
  genes";
RL Gene 144:283-287(1994).
CC -1- FUNCTION: INHIBITS SURVIVAL AND NEURITE FORMATION OF CORTICAL
  NEURONS IN VITRO.
CC -1- ONLY A NEGLIGIBLE AMOUNT OF CADMIUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M93310; AAA39529.1; -.
CC EMBL: S72046; AAB31397.1; -.
CC DR PIR: A46034; A46034.
CC DR HSP: P18055; IMRB.
CC DR MGD: M91713; M13.
CC DR InterPro: IPR003019; Metallothion.
CC DR InterPro: IPR000006; Metallothion_vert.
CC DR Pfam: PF00131; metalthio; 1.
CC DR PRINTS: PR00860; MTVERTBRATE.
CC DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
CC DR Metal-binding; Metal-Chiolate cluster; Chelation; Zinc; Copper;
  KM Acetylation.
CC FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
CC FT DOMAIN 1 30 BETA.
CC FT DOMAIN 31 68 ALPHA.
CC FT METAL 6 6 CLUSTER B (BY SIMILARITY).
CC FT METAL 8 8 CLUSTER B (BY SIMILARITY).
CC FT METAL 14 14 CLUSTER B (BY SIMILARITY).
CC FT METAL 16 16 CLUSTER B (BY SIMILARITY).
CC FT METAL 20 20 CLUSTER B (BY SIMILARITY).
CC FT METAL 22 22 CLUSTER B (BY SIMILARITY).
CC FT METAL 25 25 CLUSTER B (BY SIMILARITY).
CC FT METAL 27 27 CLUSTER B (BY SIMILARITY).
CC FT METAL 30 30 CLUSTER B (BY SIMILARITY).
CC FT METAL 34 34 CLUSTER A (BY SIMILARITY).
CC FT METAL 35 35 CLUSTER A (BY SIMILARITY).
CC FT METAL 37 37 CLUSTER A (BY SIMILARITY).
CC FT METAL 38 38 CLUSTER A (BY SIMILARITY).
CC FT METAL 42 42 CLUSTER A (BY SIMILARITY).
CC FT METAL 45 45 CLUSTER A (BY SIMILARITY).
CC FT METAL 49 49 CLUSTER A (BY SIMILARITY).
CC FT METAL 51 51 CLUSTER A (BY SIMILARITY).
CC FT METAL 64 64 CLUSTER A (BY SIMILARITY).
CC FT METAL 66 66 CLUSTER A (BY SIMILARITY).
CC FT METAL 67 67 CLUSTER A (BY SIMILARITY).
CC SQ SEQUENCE 68 AA; 7009 MW; 791AF0E38FED3CA CRC64;

```

```

RESULT 9
CRS5_YEAST STANDARD; PRT; 69 AA.
AC P41902;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE METALLOTHIONEIN-LIKE PROTEIN CRS5.
GN CRS5 OR YOR031W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014318; PubMed=7929222;
RA Colotta V.C., Howard W.R., Liu X.F.;
RT "CRS5 encodes a metallothionein-like protein in Saccharomyces
  cerevisiae";
RL J. Biol. Chem. 269:25295-25302(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / FY1679;
RA de Haan M., Maarse A.C., Grievell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CRITICAL ROLE IN COPPER (SPECIFIC) HOMEOSTASIS AND
  DETOXIFICATION. MAY PROTECT BY DIRECTLY CHELATING AND SEQUESTERING
  COPPER IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 IN METALLOTHIONEIN SUPERFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L29056; AAA6061.1; -.
CC DR EMBL: X87331; -. NOT_ANNOTATED_CDS.
CC DR SGD: S0005557; CRS5.
CC DR Metal-binding; Metal-Chiolate cluster; Chelation.
CC SQ SEQUENCE 69 AA; 7321 MW; CEEF91203A813FF4 CRC64;

Query Match 19.9%; Score 52.5; DB 1; Length 69;
Best Local Similarity 31.4%; Pred. No. 6.1;
Matches 11; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

OY 18 QTCCK-----SCKNTDSRCKARQLELNERTCCK 45
DB 31 ECKCKDHSTGSPCKSCGCKC-----FTTCCK 59

RESULT 10
MT2_COLL1 STANDARD; PRT; 63 AA.
AC P15787;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-2).
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_Taxid=9932;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90167121; PubMed=2407296;
RA Lin L.-Y., Lin W.C., Huang P.C.;

```

FT "Pleogen metallothionein consists of two species";  
 RL Blochum Biophys. Acta 1037:248-255(1990)  
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 RESIDUES THAT BIND VARIOUS HEAVY METALS.  
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:  
 FOUR DIVERGENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA  
 DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11  
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE  
 CC BETA DOMAIN, CAN LIGATE THREE DIVERGENT IONS TO 9 CYSTEINES.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.  
 DR PIR: S08191; S08191.  
 DR HSSP: P02795; 2MHU.  
 DR InterPro: IPR003019; Metallothion.  
 DR InterPro: IPR000006; Metallothion\_vert.  
 DR Pfam: PF00131; metalthio; 1.  
 DR PRINTS: PR00860; MYVERTEBRATE.  
 DR PROSITE: PS00203; METALLOTHIONEIN\_VRT; 1.  
 KW Metal-binding; Metal-thiolate cluster; Chelation.  
 FT DOMAIN 1 30  
 FT METAL 31 63 ALPHA.  
 FT METAL 6 6 CLUSTER B.  
 FT METAL 8 8 CLUSTER B.  
 FT METAL 14 14 CLUSTER B.  
 FT METAL 16 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER B.  
 FT METAL 22 22 CLUSTER B.  
 FT METAL 25 25 CLUSTER B.  
 FT METAL 27 27 CLUSTER B.  
 FT METAL 30 30 CLUSTER B.  
 FT METAL 34 34 CLUSTER A.  
 FT METAL 35 35 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT METAL 38 38 CLUSTER A.  
 FT METAL 42 42 CLUSTER A.  
 FT METAL 45 45 CLUSTER A.  
 FT METAL 49 49 CLUSTER A.  
 FT METAL 51 51 CLUSTER A.  
 FT METAL 59 59 CLUSTER A.  
 FT METAL 61 61 CLUSTER A.  
 FT METAL 62 62 CLUSTER A.  
 SQ SEQUENCE 63 AA; 6452 MW; A2B84227E94C365E CRC64;  
 QY 16 DPQCKC-----SKNTDSCKKARQLELNRTCRC 45  
 DB 2 DPQDCTCAAGDSCAGSCAGSKCKKNCQGS---CRKSCSCG 37  
 Query Match 19.7%; Score 52; DB 1; Length 63;  
 Best Local Similarity 30.0%; Pred. No. 6.5;  
 Matches 12; Conservative 4; Mismatches 10; Indels 14; Gaps 2;  
 RESULT 11  
 MT3\_HUMAN  
 ID MT3\_HUMAN STANDARD; PRT; 68 AA.  
 AC P25713;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).  
 GN MT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=92335292; PubMed=1631128;  
 RA Palmer R.D., Findley S.D., Whitmore T.E., Durman D.M.;  
 RL "MT-III, a brain-specific member of the metallothionein gene family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6333-6337(1992).  
 RN [2]

```

RP SEQUENCE FROM N.A., AND SEQUENCE
RC TISSUE=Brain:
RX MEDLINE=91337462; PubMed=1873033:
RA Uchida Y., Takio K., Tiltan K., Ihara Y., Tomonaga M.:
RT "The growth inhibitory factor that is deficient in the Alzheimer's
RL disease brain is a 68 amino acid metallothionein-like protein.";
RN Neuron 7:337-347(1991).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93099858; PubMed=1464312;
RA Tsuji S., Kobayashi H., Uchida Y., Ihara Y., Miyatake T.:
RT "Molecular cloning of human growth inhibitory factor cDNA and its
RL down-regulation in Alzheimer's disease.";
RN EMO J. 11:4843-4850(1992).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94314230; PubMed=8039715;
RA Naruse S., Igarashi S., Furuya T., Kobayashi H., Miyatake T.,
RA Tsuji S.:
RT "Structures of the human and mouse growth inhibitory factor-encoding
RL genes.";
RN Gene 144:283-287(1994).
[5]
RP SEQUENCE FROM N.A.
RA Amoureux M.C., Rethaus E., Wurch T., Colpaert F.C., Pauwels P.J.:
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: INHIBITS SURVIVAL AND NEURITE FORMATION OF CORTICAL
CC NEURONS IN VITRO.
CC -I- FUNCTION: BINDS HEAVY METALS. CONTAINS THREE ZINC AND FOUR COPPER
CC ATOMS PER POLYPEPTIDE CHAIN AND ONLY A NEGLECTIBLE AMOUNT OF
CC CADMIUM.
CC -I- TISSUE SPECIFICITY: ABUNDANT IN A SUBSET OF ASTROCYTES IN THE
CC NORMAL HUMAN BRAIN, BUT GREATLY REDUCED IN THE ALZHEIMER'S
CC DISEASE (AD) BRAIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M93311; AAA36214.1; -.
DR EMBL; D13365; -. NOT_ANNOTATED_CDS.
DR EMBL; S72043; AAB31396.1; -.
DR EMBL; X89604; CAB61763.1; -.
DR PIR; S28393; S28393.
DR PIR; B46034; B46034.
DR HSP; P18055; IMRB.
DR MIM; 139255; -.
DR InterPro: IPR003019; Metallothion.
DR InterPro: IPR000006; Metallothion_vert.
DR Pfam; PF00131; metalthio; 1.
DR PRINTS; PRO0860; MTEVERTEBRATE.
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
DR KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;
KV Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT FT 1 30 BETA.
FT DOMAIN 31 68 ALPHA.
FT METAL 6 6
FT METAL 8 8 CLUSTER B (BY SIMILARITY).
FT METAL 14 14 CLUSTER B (BY SIMILARITY).
FT METAL 16 16 CLUSTER B (BY SIMILARITY).
FT METAL 20 20 CLUSTER B (BY SIMILARITY).
FT METAL 22 22 CLUSTER B (BY SIMILARITY).
FT METAL 25 25 CLUSTER B (BY SIMILARITY).
FT METAL 27 27 CLUSTER B (BY SIMILARITY).
FT METAL 30 30 CLUSTER B (BY SIMILARITY).
FT METAL 34 34 CLUSTER A (BY SIMILARITY).
FT METAL 35 35 CLUSTER A (BY SIMILARITY).

```

FT METAL 37 37 CLUSTER A (BY SIMILARITY).  
 FT METAL 38 38 CLUSTER A (BY SIMILARITY).  
 FT METAL 42 42 CLUSTER A (BY SIMILARITY).  
 FT METAL 45 45 CLUSTER A (BY SIMILARITY).  
 FT METAL 49 49 CLUSTER A (BY SIMILARITY).  
 FT METAL 51 51 CLUSTER A (BY SIMILARITY).  
 FT METAL 64 64 CLUSTER A (BY SIMILARITY).  
 FT METAL 66 66 CLUSTER A (BY SIMILARITY).  
 FT METAL 67 67 CLUSTER A (BY SIMILARITY).  
 SQ SEQUENCE 68 AA; 6927 MW; 59801ECF5BC8A406 CRC64;

Query Match 19.7%; Score 52; DB 1; Length 68;  
 Best Local Similarity 38.2%; Pred. No. 6.9;  
 Matches 13; Conservative 2; Mismatches 7; Indels 12; Gaps 3;

QY 16 DPQCKC-----SKNTSRCKARQLEINERTC 45  
 DB 2 DPETCPGSGSGCTCADS-CRC-----ECCCK 27

RESULT 12  
 MTL\_SCYSE STANDARD; PRT; 58 AA.  
 ID MTL\_SCYSE  
 AC P02805;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE METALLOTHIONEIN-I (MT-I).  
 OS Scylla serrata (Mud crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubranchyura; Portunoidae; Portunidae; Scylla.  
 OX NCBI\_Taxid=6761;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=62142340; PubMed=7061431;  
 RA Lerch K., Ammer D., Olafson R.W.;  
 RT "Crab metallothionein. Primary structures of metallothioneins 1 and 2."  
 RT J. Biol. Chem. 257:2420-2426(1982).  
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTs IN MARINE  
 CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS  
 CC OF HEAVY-METAL IONS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.  
 CC PIR: A03283; SMKDIS.  
 DR HSP: P55949; IDMP.  
 DR InterPro: IPR003019; Metallothion.  
 DR InterPro: IPR002045; Metallothion\_crust.  
 DR Pfam: PF00131; metalthio; 1.  
 DR PRINTS: PR00858; MTCRUSTACEAN.  
 KM Metal-binding; Metal-chelolate cluster; Chelation.  
 FT DOMAIN 1 28 BETA.  
 FT METAL 29 58 ALPHA.  
 FT METAL 4 4 CLUSTER B.  
 FT METAL 5 5 CLUSTER B.  
 FT METAL 9 9 CLUSTER B.  
 FT METAL 11 11 CLUSTER B.  
 FT METAL 16 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER B.  
 FT METAL 22 22 CLUSTER B.  
 FT METAL 25 25 CLUSTER B.  
 FT METAL 27 27 CLUSTER B.  
 FT METAL 30 30 CLUSTER B.  
 FT METAL 33 33 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT METAL 39 39 CLUSTER A.  
 FT METAL 45 45 CLUSTER A.  
 FT METAL 49 49 CLUSTER A.  
 FT METAL 53 53 CLUSTER A.  
 FT METAL 55 55 CLUSTER A.  
 FT METAL 56 56 CLUSTER A.

SQ SEQUENCE 58 AA; 6001 MW; CE8A24C590B027B8 CRC64;

Query Match 19.5%; Score 51.5; DB 1; Length 58;  
 Best Local Similarity 38.5%; Pred. No. 6.9;  
 Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 19 TCKCS-CKNTDSRCKARQLEINERTC 43  
 DB 24 SCRCSPCKSGSGCKANKECSKTC 49

RESULT 13  
 IB1\_DIOGL STANDARD; PRT; 67 AA.  
 ID IB1\_DIOGL  
 AC P82469;

DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BOWMAN-BIRK TYPE PROTEINASE INHIBITOR I (DGTI).  
 OS Dioclea glabra.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dioclea.  
 OX NCBI\_Taxid=124593;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=99373165; PubMed=10441512;  
 RA Bueno N.R., Filtz H., Auerwald E.A., Mentele R., Sampaio M.U.,  
 RA Sampaio C.A.M., Oliva M.L.V.;  
 RT "Primary structure of Dioclea glabra trypsin inhibitor, DgtI, a Bowman-Birk inhibitor."  
 RT Biochem. Biophys. Res. Commun. 261:838-843(1999).  
 CC -1- FUNCTION: INHIBITS TRYPSIN BUT NOT CHYMOTRYPSIN. THE INHIBITOR  
 CC CONSISTS OF 2 DOMAINS AND HAS 2 SITES OF INTERACTION WITH TRYPSIN.  
 CC -1- SUBUNIT: MONOMER. ALTHOUGH DIMERIZATION MAY OCCUR IN SOLUTION.  
 CC -1- TISSUE SPECIFICITY: SEED.

CC -1- SIMILARITY: BELONGS TO THE BOWMAN-BIRK SERINE PROTEASE INHIBITORS  
 CC FAMILY.  
 DR InterPro: IPR000877; Bowman-Birk\_leg.  
 DR Pfam: PF00228; Bowman-Birk\_leg; 1.  
 DR ProDom: PD002168; Bowman-Birk\_leg; 1.  
 DR SMART: SM00269; BOWB; 1.

DR PROSITE: PS00281; BOWMAN BIRK; 1.  
 KM Serine protease inhibitor.  
 FT ACT\_SITE 13 13 INTERACTION WITH TRYPSIN.  
 FT ACT\_SITE 40 40 INTERACTION WITH TRYPSIN.  
 FT DISULFID 5 59 BY SIMILARITY.  
 FT DISULFID 6 21 BY SIMILARITY.  
 FT DISULFID 9 55 BY SIMILARITY.  
 FT DISULFID 11 19 BY SIMILARITY.  
 FT DISULFID 29 36 BY SIMILARITY.  
 FT DISULFID 33 48 BY SIMILARITY.  
 FT DISULFID 38 46 BY SIMILARITY.  
 SQ SEQUENCE 67 AA; 7242 MW; EDYCABCB8A9F57B1 CRC64;

Query Match 19.5%; Score 51.5; DB 1; Length 67;  
 Best Local Similarity 25.0%; Pred. No. 7.8;  
 Matches 12; Conservative 8; Mismatches 11; Indels 17; Gaps 3;

QY 3 GPCEERKHLFVDPQCKSCSKNTDSRCKARQLEINERTC 45  
 DB 3 GPCCDR-----CRCT-KSEPPQCCQDVRLNSCHSACEACVC 38

RESULT 14  
 MT3\_BOVIN STANDARD; PRT; 68 AA.  
 ID MT3\_BOVIN  
 AC P37359;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).  
GN MT3.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OX Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94259179; PubMed=8200454;  
RA Pountney D.L., Fundel S.M., Fallier P., Birchler N.E., Hunziker P.,  
RA Vasak M.;  
RT "Isolation, primary structures and metal binding properties of  
RT neuronal growth inhibitory factor (GIF) from bovine and equine  
RT brain.";  
RL FEBS Lett. 345:193-197(1994).  
CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS FIVE ZINC AND ONE COPPER  
CC ATOMS PER POLYPEPTIDE CHAIN AND ONLY A NEGLIGIBLE AMOUNT OF  
CC CADMIUM.  
CC -1- TISSUE SPECIFICITY: BRAIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.  
CC PIR, S44391; S44391.  
DR HSSP; P18055; IMRB.  
DR InterPro; IPR003019; Metallothion.  
DR InterPro; IPR000006; Metallothion\_vert.  
DR Pfam; PF00131; metalthio; 1.  
DR PRINTS; PR00860; MVTERTERRATE.  
DR PROSITE; PS00203; METALLOTHIONEIN\_VRT; 1.  
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;  
KW Acetylation.  
FT MOD\_RES 1 1 ACETYLATION.  
FT FT DOMAIN 1 1 30 BETA.  
FT FT METAL 31 68 ALPHA.  
FT METAL 8 6 CLUSTER B (BY SIMILARITY).  
FT METAL 8 8 CLUSTER B (BY SIMILARITY).  
FT METAL 14 14 CLUSTER B (BY SIMILARITY).  
FT METAL 16 16 CLUSTER B (BY SIMILARITY).  
FT METAL 20 20 CLUSTER B (BY SIMILARITY).  
FT METAL 22 22 CLUSTER B (BY SIMILARITY).  
FT METAL 25 25 CLUSTER B (BY SIMILARITY).  
FT METAL 27 27 CLUSTER B (BY SIMILARITY).  
FT METAL 30 30 CLUSTER B (BY SIMILARITY).  
FT METAL 34 34 CLUSTER A (BY SIMILARITY).  
FT METAL 35 35 CLUSTER A (BY SIMILARITY).  
FT METAL 37 37 CLUSTER A (BY SIMILARITY).  
FT METAL 38 38 CLUSTER A (BY SIMILARITY).  
FT METAL 42 42 CLUSTER A (BY SIMILARITY).  
FT METAL 45 45 CLUSTER A (BY SIMILARITY).  
FT METAL 49 49 CLUSTER A (BY SIMILARITY).  
FT METAL 51 51 CLUSTER A (BY SIMILARITY).  
FT METAL 64 64 CLUSTER A (BY SIMILARITY).  
FT METAL 66 66 CLUSTER A (BY SIMILARITY).  
FT METAL 67 67 CLUSTER A (BY SIMILARITY).  
SQ SEQUENCE 68 AA; 6953 MW; FC824B83AA52B4C0 CRC64;

Query Match 19.3%; Score 51; DB 1; Length 68;  
Best Local Similarity 29.6%; Pred. No. 9;  
Matches 16; Conservative 4; Mismatches 16; Indels 18; Gaps 4;

OY 1 PC---GPCSRKRLHLPDPOGK-----SKNTDSRCAROLELNERCRC 45  
DB 7 PCPTGGSGCT-----CSDP--CKEGCTCAACKSCCSCCPAECCKACADVC 51

RESULT 15  
MT3 HORSE STANDARD; PRT; 68 AA.  
AC P37360;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).  
GN MT3.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94259179; PubMed=8200454;  
RA Pountney D.L., Fundel S.M., Fallier P., Birchler N.E., Hunziker P.,  
RA Vasak M.;  
RT "Isolation, primary structures and metal binding properties of  
RT neuronal growth inhibitory factor (GIF) from bovine and equine  
RT brain.";  
RL FEBS Lett. 345:193-197(1994).  
CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS THREE ZINC AND THREE COPPER  
CC ATOMS PER POLYPEPTIDE CHAIN AND ONLY A NEGLIGIBLE AMOUNT OF  
CC CADMIUM.  
CC -1- TISSUE SPECIFICITY: BRAIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.  
CC PIR, S44392; S44392.  
DR HSSP; P18055; IMRB.  
DR InterPro; IPR003019; Metallothion.  
DR InterPro; IPR000006; Metallothion\_vert.  
DR Pfam; PF00131; metalthio; 1.  
DR PRINTS; PR00860; MVTERTERRATE.  
DR PROSITE; PS00203; METALLOTHIONEIN\_VRT; 1.  
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;  
KW Acetylation.  
FT MOD\_RES 1 1 ACETYLATION.  
FT FT DOMAIN 1 1 30 BETA.  
FT FT METAL 31 68 ALPHA.  
FT METAL 8 6 CLUSTER B (BY SIMILARITY).  
FT METAL 8 8 CLUSTER B (BY SIMILARITY).  
FT METAL 14 14 CLUSTER B (BY SIMILARITY).  
FT METAL 16 16 CLUSTER B (BY SIMILARITY).  
FT METAL 20 20 CLUSTER B (BY SIMILARITY).  
FT METAL 22 22 CLUSTER B (BY SIMILARITY).  
FT METAL 25 25 CLUSTER B (BY SIMILARITY).  
FT METAL 27 27 CLUSTER B (BY SIMILARITY).  
FT METAL 30 30 CLUSTER B (BY SIMILARITY).  
FT METAL 34 34 CLUSTER A (BY SIMILARITY).  
FT METAL 35 35 CLUSTER A (BY SIMILARITY).  
FT METAL 37 37 CLUSTER A (BY SIMILARITY).  
FT METAL 38 38 CLUSTER A (BY SIMILARITY).  
FT METAL 42 42 CLUSTER A (BY SIMILARITY).  
FT METAL 45 45 CLUSTER A (BY SIMILARITY).  
FT METAL 49 49 CLUSTER A (BY SIMILARITY).  
FT METAL 51 51 CLUSTER A (BY SIMILARITY).  
FT METAL 64 64 CLUSTER A (BY SIMILARITY).  
FT METAL 66 66 CLUSTER A (BY SIMILARITY).  
FT METAL 67 67 CLUSTER A (BY SIMILARITY).  
SQ SEQUENCE 68 AA; 6927 MW; 5998E0F17FC52CE6 CRC64;

Query Match 19.3%; Score 51; DB 1; Length 68;  
Best Local Similarity 24.0%; Pred. No. 9;  
Matches 12; Conservative 4; Mismatches 14; Indels 20; Gaps 1;

OY 16 DPOTGCK-----SKNTDSRCAROLELNERCRC 45  
DB 2 DPETCPPTGGSGCTGCGCKGCKYCKKSCCSCCPAECCKACADVC 51

Search completed: January 31, 2002, 11:22:32  
Job time: 113 sec

**THIS PAGE BLANK (USPTO)**

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:19:34 ; Search time 13.28 Seconds

(without alignments)  
258.122 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264  
Sequence: 1 PCGPCSRRKRLFLVQDPQTC.....NTDSRCKARQLELNERTC 45

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 30440

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_68:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	22.0	83	2	D84697
2	54	20.5	75	2	B45206
3	53.5	20.3	63	2	A34905
4	53.5	20.3	74	2	T24715
5	53	20.1	62	2	I51538
6	53	20.1	63	2	C34620
7	53	20.1	63	2	S33381
8	53	20.1	63	2	A34620
9	53	20.1	63	2	A34958
10	53	20.1	66	2	S58086
11	53	20.1	68	2	A46034
12	53	20.1	68	2	I67866
13	52.5	19.9	69	2	A55011
14	52	19.7	63	2	S08191
15	52	19.7	68	2	B46034
16	51.5	19.5	58	1	SMKDIS
17	51.5	19.5	83	2	A05157
18	51	19.3	68	2	S44392
19	51	19.3	68	2	S44391
20	51	19.3	68	2	JC6521
21	51	19.3	75	2	S17156
22	51	19.3	91	2	S71147
23	49.5	18.8	35	1	S59072
24	49	18.6	35	1	NTSRPM
25	49	18.6	96	2	E64505
26	48.5	18.4	87	2	A39439
27	48.5	18.4	98	2	T43349
28	48	18.2	57	2	S59073
29	48	18.2	81	2	T14444

30	48	18.2	88	2	JC5203	outer membrane pro
31	47.5	18.0	35	2	A24677	Balbani ring 2 ch
32	47.5	18.0	62	2	A53640	metallochionein 2
33	47.5	18.0	71	2	S47576	metallochionein 20
34	47.5	18.0	71	2	S39420	metallochionein 20
35	47.5	18.0	82	1	TIZBI	protease inhibi
36	47.5	18.0	84	2	A61594	thrombospondin - b
37	47.5	18.0	92	2	A72242	ferredoxin - Therm
38	47	17.8	57	1	SMKDS	metallochionein 2
39	47	17.8	62	2	S15676	chorionic gonadot
40	46.5	17.6	95	2	S01717	Balbani ring prot
41	46	17.4	50	2	S53431	echistatin beta -
42	46	17.4	52	2	JC1197	metallochionein II
43	46	17.4	58	2	S43367	metallochionein -
44	46	17.4	70	2	T13341	hypothetical prote
45	46	17.4	72	2	S39416	metallochionein 10

#### ALIGNMENTS

RESULT 1  
D84697  
hypothetical protein At2g29530 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: D84697  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shua, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Taitler,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420, MUID:20083487  
A:Accession: D84697  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-83 <STO>  
A:Cross-references: GB:AE002093; NID:g3980383; PIDN:AAC95186.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g29530  
A:Map position: 2

Query Match 22.0%; Score 58; DB 2; Length 83;  
Best Local Similarity 39.0%; Pred. No. 11;  
Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

QY 7 ERRKHLFVQDPQTCCKNTDSRCKARQLELNERTC--RC 45  
DB 23 EYRVELFNKLAQTCFNKC--VDKRYKEALNMGENSEIDRC 61

RESULT 2  
B45206  
metallochionein 2 - Caenorhabditis elegans  
N:Alternate names: metallochionein I  
C:Species: Caenorhabditis elegans  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 29-Oct-1999  
C:Accession: B45206; S09714; T29721  
R:Freeman, J.H.; Slice, L.W.; Dixon, D.; Fire, A.; Rubin, C.S.  
J. Biol. Chem. 268, 2554-2564, 1993  
A:Title: The novel metallochionein genes of Caenorhabditis elegans. Structural organi  
A:Reference number: A45206; MUID:93155063  
A:Accession: B45206  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-75 <PRE>  
A:Note: sequence extracted from NCBI backbone (NCBI:124147)  
R:Imagawa, M.; Onozawa, T.; Okumura, K.; Osada, S.; Nishihara, T.; Kondo, M.  
Biochem. J. 268, 237-240, 1990  
A:Title: Characterization of metallochionein cDNAs induced by cadmium in the nematode  
A:Reference number: S09714; MUID:90262552  
A:Accession: S09714

A:Molecule type: mRNA  
A:Residues: 1-75 <IMA>  
A:Cross-references: EMBL:X53244; NID:g6779; PIDN:CAA37334.1; PID:g6780  
R:Greco, T.; Bradshaw, H.  
Submitted to the EMBL data library, July 1996  
A:Description: The sequence of *C. elegans* cosmid K11G9.  
A:Reference number: Z20672  
A:Accession: J29721  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-75 <GR>  
A:Cross-references: EMBL:U64853; PIDN:AA04979.1; GSPDB:GNO0023; CESP:K11G9.6  
A:Experimental source: strain Bristol N2; clone K11G9  
C:Genetics:  
A:Gene: CESP:K11G9.6  
A:Map position: 5  
A:Introns: 6/1  
C:Superfamily: metallochionein

Query Match	20.5%	Score 54	DB 2	Length 75
Best Local Similarity	34.6%	Pred. No. 28		
Matches	9	Conservative	2	Mismatches 7; Indels 8; Gaps 1
Qy	20	CKCSCKNITDSRCKARQLEINERTCNC	45	
Db	3	CKCDCKNKCKCKGDK-----CNC	20	

RESULT 3  
A34905  
metallothionein 1 - Caenorhabditis elegans  
N:Alternate names: metallothionein Ce; metallothionein II  
C:Species: Caenorhabditis elegans  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
A:Accession: A45206; A34905; S09715  
J:Freeman, J.H.; Slice, L.W.; Dixon, D.; Fire, A.; Rubin, C.S.  
J Biol. Chem. 268, 2554-2564, 1993  
A>Title: The novel metallothionein genes of Caenorhabditis elegans. Structural organization  
A:Reference number: A45206; MUID:9155063  
A:Accession: A45206  
A>Status: preliminary: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-63 <FE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:124145)  
R:Slice, L.W.; Freeman, J.H.; Rubin, C.S.  
J. Biol. Chem. 265, 256-263, 1990  
A>Title: Purification, characterization, and cDNA cloning of a novel metallothionein-1-like  
A:Reference number: A34905; MUID:90094407  
A:Accession: A34905  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-63 <SLI>  
A:Cross-references: GB:M32386; NID:g156380; PIDN:AAA28117.1; PID:g156381; GB:J05169  
A:Imagawa, M.; Onozawa, T.; Okumura, K.; Osada, S.; Nishihara, T.; Kondo, M.  
Biochem. J. 268, 237-240, 1990  
A>Title: Characterization of metallothionein cDNAs induced by cadmium in the nematode Caenorhabditis elegans  
A:Reference number: S09714; MUID:90262552  
A:Accession: S09715  
A:Molecule type: mRNA  
A:Residues: 1-63 <IMA>  
A:Cross-references: EMBL:X53245; NID:g6781; PIDN:CAA37335.1; PID:g6782  
A:Superfamily: metallothionein

Query Match	20.38;	Score 53.5;	DB 2;	length 63;
Best Local Similarity	34.68;	Pred. No. 28;		
Matches	9;	Conservative	2;	Mismatches 10;
				Indels 5;
				Gaps 1.

```

QY      20 CKSCKNNTDSRCKARQLEINERTCRC 45
          ||| ||| : | : |||
DB      3  CKCDCKNQNCSCNT-----GTKDCDC 23

```

```

RESULT      4
T247715
hypothetical protein T08G5.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T247715
R:Smey, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19927
A:Accession: T247715
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-74 <WILD>
A:Cross-references: EMBL:Z81589; PIDDN:CAB04723.1; GSPDB:GNO0023; CESP:T08G5.10
A:Experimental source: clone T08G5
C:Genetics:
A:Gene: CESP:T08G5.10
A:Map position: 5
A:Introns: 17/1
C:Superfamily: metallothionein

Query Match      20.3%   Score 53.5; DB 2; Length 74;
Best Local Similarity 34.6%; Pred No. 31;
Matches 9; Conservative 2; Mismatches 10; Indels 5; Gaps 1

```

RESULT 5  
151538  
metallothionein - African clawed frog  
C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Aug-1999  
C:Accession: 151538  
R:Saint-Jacques, E.; Seguin, C.  
DNA Cell Biol. 12, 329-340, 1993  
A:Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis  
A:Reference number: 151538; MUID:93263990  
A:Accession: 151538  
A:Status: preliminary; translated from GR/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-62 <SA>  
A:Cross-references: NID:g214585; PTDN:AMB59949.1; PID:g214586  
C:Superfamily: metallothionein

Query Match	20.1%	Score 53	DB 2	Length 62	
Best Local Similarity	33.3%	Pred. No. 31			
Matches	12	Conservative	2	Mismatches 16	
				Indels 6	
				Gaps 1	
OY	16	DPOTCK-----C	SCKNND	SRCAQALELNE	ETCRIC 45
Db	2	DPDQCKETG	ASCSCG	TTTSCSN	CKCTSC
					KKKCCSC 37

```

RESULT      6
C34620
metallothionein - muscovy duck
C:Species:  Cairina moschata (muscovy duck)
C:Date:      22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C:Accession: C34620; JC5094
R:Lin, L.Y.; Huang, P.C.
Biochem. Biophys. Res. Commun. 168, 182-187, 1990
A:Title: Complete homology in metallothionein from two genera of ducks and their hybrid
A:Reference number: A34620; MUID:90226357
A:Accession: C34620
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <LIN>

```



R:Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.  
Gene 176, 85-92, 1996  
A:Title: Structure and expression of metallothionein gene in ducks.  
A:Reference number: JC5094; MUID:97075914  
A:Accession: JC5094  
A:Molecule type: mRNA  
A:Residues: 1-63 <LEE>  
A:Cross\_references: GB:U34230; NID:g1000297; PIDN:AAC0047.1; PID:g1000298  
C:Comment: This protein has a high metal binding capacity and sulfur content.  
C:Genetics:  
A:Gene: mt  
A:Introns: 11/1; 33/1  
C:Superfamily: metallothionein

Query Match	20.1%;	Score 53;	DB 2;	Length 63;
Best Local Similarity	30.0%;	Pred. NO. 31;		
Matches 12; Conservative	4;	Mismatches 10;	Indels 14;	Gaps 2;

```

QY 16 DPQTKC-----SKRTIDRCARQLELNEKRC 45
      ||| |      ||| : ||| : | |
Db 2 DPQDTCAAGDSCSCAGSCCKCKNCRCNS---CRKSCCSC 37

```

RESULT 7  
S33381  
metallothionein - turkey  
C:Species: Meleagris galllopavo (common turkey)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S33381; S33380; S18180  
R:Shartzer, K.L.; Kage, K.; Sobleski, R.J.; Andrews, G.K.  
J. Mol. Evol. 36, 255-262, 1993  
A:Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metalld  
A:Reference number: S33378; MUID:93247066  
A:Accession: S33381  
A:Molecule type: DNA  
A:Residues: 1-63 <SHA>  
A:Cross-references: EMBL:X62513  
A:Accession: S33380  
A:Molecule type: mRNA  
A:Residues: 15-57 <SH2>  
A:Cross-references: EMBL:X62514; NID:g64090; PIDN:CAAA4372.1; PID:g64091  
C:Genetics:  
A:Introns: 11/1, 33/1  
C:Superfamily: metallothionein

Query Match	20.1%;	Score 53;	DB 2;	Length 63;
Best Local Similarity	30.0%;	Pred. NO. 31;		
Matches 12; Conservative	4;	Mismatches 10;	Indels 14;	Gaps 2;

```

QY      16 DPQTKC-----SCKNTDSRCARQLELNEKTRC 45
      ||| | | ||| : ||:: : | |
Db      2 DPQDCTCAAGDSCSCAGSCCKNCRCRS----CRKSCCSC 37

```

RESULT 8  
A34620  
metallothionein - duck  
C:Species: Anas platyrhynchos (domestic duck)  
C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 20-Aug-1999  
C:Accession: A34620; B34620; S13154; JC5095  
R:Llin, L.Y.; Huang, P.C.  
Biochem. Biophys. Res. Commun. 168, 182-187, 1990  
A:Title: Complete homology in metallothionein from two genera of ducks and their hybrids  
A:Reference number: A34620; M0ID:90226357  
A:Accession: A34620  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-63 <LIN>  
A:Experimental source: Anas platyrhynchos (domestic duck)  
A:Accession: B34620  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-63 <LI2>  
A:Experimental source: *Anas platyrhynchos* x *Carina moschata* (domestic duck x muscovy duck)  
A:BioRxn, L.Y.; Liu, L.F.; Tam, M.F.; Huang, P.C.; Vestling, M.; Fenselau, C. *Biochim. Biophys. Acta* 1041, 31-35, 1990  
A:Title: Primary sequence of duck metallochionein.  
A:Reference number: S13154; MUID:91027866  
A:Accession: S13154  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-63 <LI3>  
A:Rhee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y. *Gene* 176, 85-92, 1996  
A:Title: Structure and expression of metallochionein gene in ducks.  
A:Reference number: J05094; MUID:97075914

A:Cross-references: GB:U34231; NID:g1000299; PID:M6C6048.1; PID:g1000300  
A:Experimental source: strain tsai ya duck  
C:Comment: This protein has a high metal binding capacity and sulfur content.  
C:Genetics:  
A:Gene: mt  
A:Introns: 11/1; 33/1  
C:Superfamily: metallothionein

```

QY      16 DPQTKC-----SCKWTDSRCARQELNERTCR 45
      ||| |      ||| : ||: : || |
Db      2 DPQDCTCAAGDSCSCAGSCCKKNCRCRS----CRKSCCSC 37

```

RESULT 9

A34958  
metallothionein - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: A34958; S01750; J00030; A28113  
R:Fernando, L.P.; Wei, D.; Andrews, G.K.  
J. Nutr. 119, 309-316, 1989  
A>Title: Structure and expression of chicken metallothionein.  
A:Reference number: A34958; MUID:89141100  
A:Accession: A34958  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-63 <FER>  
R:Wei, D.; Andrews, G.K.  
Nucleic Acids Res. 16, 537-553, 1988  
A>Title: Molecular cloning of chicken metallothionein. Deduction of the complete amino  
A:Reference number: S01750; MUID:88124253  
A:Accession: S01750  
A:Molecule type: mRNA  
A:Residues: 1-63 <WEI>  
A:Cross-references: EMBL:X06749; NID:963617; PIDN:CAA29924.1; PID:963618  
A>Note: part of this sequence, including the amino end of the mature protein, was con  
R:Fernando, L.P.; Andrews, G.K.  
Gene 81, 177-183, 1989  
A>Title: Cloning and expression of an avian metallothionein-encoding gene.  
A:Reference number: J00030; MUID:90034180  
A:Accession: J00030  
A:Molecule type: DNA  
A:Residues: 1-63 <FE2>  
R:McCormick, C.C.; Fullmer, C.S.; Garvey, J.S.  
Proc. Natl. Acad. Sci. U.S.A. 85, 309-313, 1988  
A>Title: Amino acid sequence and comparative antigenicity of chicken metallothionein.  
A:Reference number: A28113; MUID:88124831  
A:Accession: A28113  
A:Molecule type: Protein  
A:Residues: 1-63 <MCC>



**A;Description:** involved in copper homeostasis and detoxification

Query Match	19.9%	Score 52.5;	DB 2;	Length 69;
Best Local Similarity	31.4%;	Pred. No. 38;		
Matches	11; Conservative	3; Mismatches	8; Indels	13; Gaps 2

```

py 18 QMKC-----SKNTDSRCKAQLNERTCRC 45
    : ||| ||: || |||
db 31 EKCKDHTGSPQCKSGEKCK-----ETTCTC 59

```

RESULT 14

metallothionein2 - pigeon  
C:Species: *Columba livia* (domestic pigeon)  
C:Date: 30-Sep-1991 #sequence\_reviston 30-Sep-1991 #text\_change 24-Nov-1999  
C:Accession: S08191  
R:Lin, L.Y.; Lin, W.C.; Huang, P.C.  
Biochim. Biophys. Acta 1037, 248-255, 1990  
A:Title: Pigeon metallothionein consists of two species.  
A:Reference number: S08190; MUID:90167121  
A:Accession: S08191  
A:Molecule type: protein  
A:Residues: 1-63 <LIN>  
C:Superfamily: metallothionein  
C:Keywords: blocked amino end  
F:1/Modified site: blocked amino end (Met) (probably acetylated) #status experimental

Query Match	19.7%;	Score 52;	DB 2;	Length 63;
Best Local Similarity	30.0%;	Pred. No. 40;		
Matches 12; Conservative	4;	Mismatches 10;	Indels 14;	Gaps 2

```

0y 16 DPQTC-----SKNTDSCKARQLENERC 45
    ||| |      ||| : || : ||
Db 2 DPQDCTCAAGDSCSCAGSCCKNCRQS---CRKSCSC 37

```

RESULT	15
DATE	03/03/2024

metallothionein3, brain-specific - human  
N:Alternate names: growth inhibitory factor; metallothionein MT-III  
C:Species: Homo sapiens (man)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Aug-1999  
C:Accession: B46034; S28393; JH0463; S58084; I33803  
R:Palmiter, R.D.; Findley, S.D.; Whitmore, T.E.; Durram, D.M.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6333-6337, 1992  
A:Title: MT-III, a brain-specific member of the metallothionein gene family.  
A:Reference number: B46034; MUID:92335292  
A:Accession: B46034  
A:Molecule type: DNA  
A:Residues: 1-68 <PAL>  
A:Cross-references: GB:93311; NID:g187546; PIDN:AAA36214.1; PID:g187547  
A:Note: Sequence extracted from NCBI Backbone (NCBIN:108717, NCBIN:111117, NCBIP:108718)  
R:Tsujii, S.; Kobayashi, H.; Uchida, Y.; Ihara, Y.; Miyatake, T.  
EMBO J. 11, 4843-4850, 1992  
A:Title: Molecular cloning of human growth inhibitory factor cDNA and its down-regulation  
A:Reference number: S28393; MUID:9309858  
A:Accession: S28393  
A:Molecule type: mRNA  
A:Residues: 1-68 <TSU>  
A:Cross-references: EMBL:D13365  
R:Uchida, Y.; Takio, K.; Tlcanl, K.; Ihara, Y.; Tomonaga, M.  
Neuron 7, 337-347, 1991  
A:Title: The growth inhibitory factor that is deficient in the Alzheimer's disease brain  
A:Reference number: JH0463; MUID:91337462  
A:Accession: JH0463  
A:Molecule type: Protein  
A:Residues: 1-68 <UCH>  
A:Note: the amino end was shown to be blocked  
R:Amouraux, M.C.; Rehsaus, E.; Much, T.; Colpaert, F.C.; Pauwels, P.J.  
submitted to the EMBL Data Library, July 1995

A;Reference number: S58084

A;Accession: S58084

A;Status: preliminary

A; molecule type: mRNA

A;Residues: 1-68 <AMO

A; Cross-references: EMBL: X89504; NID: g914850; PIDN: CAA61763.1; PID: g914851  
R.Naruse, S.; Igarashi, S.; Furuya, T.; Kobayashi, H.; Miyatake, T.; Tsuji, S

Gene 144, 283-287, 1994

A; Reference number: I53803; MUID: 94314230

A;Accession: 153803

A; Status: preliminary; translated from GB/EMBL/DBJ

A; molecule type: DNA

A;Residues: 1-68 <RES

A;Cross-references: GB:S72043; NID:g565189; PIDN:AAB31396.1; PID:g565190

C;Genetics:  
A:Gene: GDB:MT3: CTE

A;Gene: GDB:M13; GLE  
A:Cross-references:

A:Map position: 16a13-16a13  
A;Cross-references: GDB:13416; OMIM:139253

```
A;Map position: 16q13-16q13
A;Introns: 11/1: 33/1
```

A; IL10: 11/1; 33/1  
C: Superfamily: metalloproteinase

**C; Keywords:** Alzheimer's disease

C:\newmotos: ATZHEHMEHET 5 URBESAC; DIOCHEN AMTHO ENH; DIAU

Query Match	19.7%	Score 52:	DB: 2:	Length 68:
Best Local Similarity	38.2%	Pred. No. 42:		
Matches 13, Conservative	2:	Mismatches 7:	Indels 12:	Gaps 3

```

QY      16 DPQTKC-----SKNTDSRCARQLELNERTCRC 45
          ||: || |      || || ||
Db      2 DPETPCPCSGSCTCADS-CRC-----EGCKC 27

```

Search completed: January 31, 2002, 11:21:47  
Job time: 133 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:19:09 ; Search time 12.47 Seconds

(without alignments)  
81.207 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264  
Sequence: 1 PCGPCSERRRKHLFVQDPQTC.....NTDSRCARQLEINERTCRC 45

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 162600

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	43.6	55	1	US-08-469-427A-3
2	115	43.6	55	2	US-08-609-443B-3
3	115	43.6	55	2	US-08-569-063C-3
4	105	39.8	18	3	US-08-807-992B-28
5	100	37.9	17	3	US-08-807-992B-29
6	76	28.8	19	3	US-08-807-992B-7
7	76	28.8	19	3	US-08-807-992B-13
8	76	28.8	19	3	US-08-807-992B-16
9	76	28.8	19	3	US-08-807-992B-30
10	52	19.7	68	1	US-07-696-051B-1
11	52	19.7	68	1	US-07-924-063A-1
12	52	19.7	68	1	US-08-138-340B-2
13	52	19.7	97	2	US-08-726-306A-18
14	50	18.9	49	4	US-09-020-880-14
15	50	18.9	49	4	US-09-020-880-16
16	48	18.2	49	4	US-09-020-880-18
17	48	18.2	49	4	US-08-226-264-22
18	47.5	18.0	26	1	US-08-138-340B-3
19	47	17.8	53	4	US-08-284-923-2
20	47	17.8	53	4	US-08-619-032B-2
21	47	17.8	100	3	US-08-965-903B-11
22	46.5	17.6	86	2	US-08-465-380-45
23	46.5	17.6	86	2	US-08-486-397-45
24	46.5	17.6	86	2	US-08-486-399-45
25	46.5	17.6	86	2	US-08-461-965-45
26	46.5	17.6	86	2	US-08-634-641-45
27	46.5	17.6	86	3	US-09-249-471-45

28	46.5	17.6	86	3	US-09-249-472-45	Sequence 45, Appl
29	46.5	17.6	86	3	US-09-249-451-45	Sequence 45, Appl
30	46.5	17.6	86	3	US-08-809-455-45	Sequence 45, Appl
31	46.5	17.6	86	3	US-09-249-461-45	Sequence 45, Appl
32	46.5	17.6	86	3	US-09-249-448-45	Sequence 45, Appl
33	46	17.4	53	6	5332668-2	Patent No. 5332669
34	46	17.4	58	3	US-08-904-446A-14	Sequence 14, Appl
35	46	17.4	76	4	US-08-866-545-4	Sequence 4, Appl
36	45.5	17.2	48	2	US-08-465-794-3	Sequence 3, Appl
37	45.5	17.2	48	3	US-09-049-813-3	Sequence 3, Appl
38	45.5	17.2	56	4	US-08-866-545-10	Sequence 10, Appl
39	45.5	17.2	58	3	US-08-904-446A-15	Sequence 15, Appl
40	45.5	17.2	61	2	US-08-453-051-2	Sequence 2, Appl
41	45.5	17.2	73	1	US-08-379-538-7	Sequence 3, Appl
42	45.5	17.2	80	4	US-08-663-191A-3	Sequence 2, Appl
43	45.5	17.2	80	4	US-09-051-624A-2	Sequence 46, Appl
44	45.5	17.2	86	2	US-08-465-380-45	Sequence 46, Appl
45	45.5	17.2	86	2	US-08-486-397-46	Sequence 46, Appl

#### ALIGNMENTS

RESULT 1  
US-08-469-427A-3  
; Sequence 3, Application US/08469427A  
; Patent No. 5607918  
; GENERAL INFORMATION:  
; APPLICANT: Eriksson, Ulf  
; APPLICANT: Olofsson, Birgitta  
; APPLICANT: Allitalo, Kari  
; APPLICANT: Pajusola, Katri  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND  
; TITLE OF INVENTION: DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
; STREET: 1200 G Street, N.W., Suite 700  
; CITY: Washington  
; STATE: DC  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,427A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/397,651  
; FILING DATE: 01-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Joseph D  
; REGISTRATION NUMBER: 26,269  
; REFERENCE/DOCKET NUMBER: 41979cp2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-8800  
; TELEFAX: (202) 628-8844  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 55 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: mouse embryo  
; US-08-469-427A-3



```

? TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
? TITLE OF INVENTION: vessel
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: David Prashker, Esq.
? STREET: P.O. Box 5387
? CITY: Magnolia
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 01930
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
? COMPUTER: IBM PS/1
? OPERATING SYSTEM: MS DOS
? SOFTWARE: Wordperfect version 5.1
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/807,992B
? FILING DATE: March 3, 1997
? CLASSIFICATION: 424
?
? ATTORNEY/AGENT INFORMATION:
? NAME: David Prashker, Esq.
? REGISTRATION NUMBER: 29,693
? REFERENCE/DOCKET NUMBER: BIS-033
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (978) 525-3794
? INFORMATION FOR SEQ ID NO: 28:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 18 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FRAGMENT TYPE: internal
?
? US-08-807-992B-28

```

RESULT 5  
US-08-807-992B-29  
Sequence 29, Application US/08807992B  
Patent No. 6022541  
GENERAL INFORMATION:  
APPLICANT: Senger, Donald R  
APPLICANT: Dvorak, Harold F  
TITLE OF INVENTION: Immunological preparation for concurrent  
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
TITLE OF INVENTION: vessel  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: IBM PS/1  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/807,992B  
FILING DATE: March 3, 1997  
CLASSIFICATION: 424

```

ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BJS-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
?
?
?
US-08-807-992B-29

Query Match 37.9% Score 100; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 OTCKCKSKNTDSRCKAR 34
|||||
Db 1 OTCKCKSKNTDSRCKAR 17

```

```

Query Match          37.9%; Score 100; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches      17; Conservative    0; Mismatches     0; Indels       0; Gaps        0;

QY      18 QTCCKSCKNTRDSRCKAR 34
         |||||
Db       1 QTCCKSCKNTRDSRCKAR 17

RESULT      6
US-08-807-992B-7
; Sequence 7, Application US/08807992B
; Patent No. 6022541
; GENERAL INFORMATION:
; APPLICANT: Senger, Donald R
; APPLICANT: Dvorak, Harold F
; TITLE OF INVENTION: Immunological preparation for concurrent
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
; TITLE OF INVENTION: permeability factor bound In-vivo to a tumor associated bio
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,992B
; FILING DATE: March 3, 1997
; CLASSIFICATION: 42A
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-807-992B-7

Query Match          28.8%; Score 76; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches      14; Conservative    0; Mismatches     0; Indels       0; Gaps        0;

```

QY 32 KAROLELNEBTCRC 45  
DB 1 KAROLELNEBTCRC 14

## RESULT 7

US-08-807-992B-13  
Sequence 13, Application US/08807992B  
Patent No. 6022541  
GENERAL INFORMATION:  
APPLICANT: Senger, Donald R  
APPLICANT: Dvorak, Harold F  
TITLE OF INVENTION: Immunological preparation for concurrent  
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: IBM PS/1  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/807,992B  
FILING DATE: March 3, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEO ID NO: 13;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-807-992B-13

Query Match 28.8%; Score 76; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0066;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KAROLELNEBTCRC 45  
DB 1 KAROLELNEBTCRC 14

RESULT 8  
US-08-807-992B-16  
Sequence 16, Application US/08807992B  
Patent No. 6022541  
GENERAL INFORMATION:  
APPLICANT: Senger, Donald R  
APPLICANT: Dvorak, Harold F  
TITLE OF INVENTION: Immunological preparation for concurrent  
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia

STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: IBM PS/1  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/807,992B  
FILING DATE: March 3, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEO ID NO: 16;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-807-992B-16

Query Match 28.8%; Score 76; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0066;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 KAROLELNEBTCRC 45  
DB 1 KAROLELNEBTCRC 14

RESULT 9  
US-08-807-992B-30  
Sequence 30, Application US/08807992B  
Patent No. 6022541  
GENERAL INFORMATION:  
APPLICANT: Senger, Donald R  
APPLICANT: Dvorak, Harold F  
TITLE OF INVENTION: Immunological preparation for concurrent  
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated bio  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David Prashker, Esq.  
STREET: P.O. Box 5387  
CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: IBM PS/1  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/807,992B  
FILING DATE: March 3, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: BIS-033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEO ID NO: 30;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids



TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-807-992B-30

Query Match 28.8%; Score 76; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.0066;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy - 32 KAROLELNERTCRC 45  
Db 1 KAROLELNERTCRC 14

RESULT 10  
US-07-696-051B-1  
Sequence 1, Application US/07696051B  
Patent No. 5214031  
GENERAL INFORMATION:  
APPLICANT: Tsuji, Shoji  
APPLICANT: Miyatake, Tadashi  
APPLICANT: Uchida, Yoko  
APPLICANT: Ihara, Yasuo  
TITLE OF INVENTION: GROWTH-INHIBITORY FACTOR AND CDNA CODING  
TITLE OF INVENTION: FOR GROWTH-INHIBITORY FACTOR  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jordan B. Bierman, BIERMAN AND MUSERLIAN  
STREET: 757 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/696,051B  
FILING DATE: 19910506  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 119620/1990  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 410164/1990  
FILING DATE: 13-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 410165/1990  
FILING DATE: 13-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Bierman, Jordan B.  
REGISTRATION NUMBER: 18,629  
REFERENCE/DOCKET NUMBER: TSU-16  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)752-7550  
TELEFAX: (212)888-6426  
TELEX: PATENILAW (VIA ITT)  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Cerebral cortex

FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..68  
OTHER INFORMATION: /note="Growth inhibitory activity  
OTHER INFORMATION: on brain cells"  
US-07-696-051B-1

Query Match 19.7%; Score 52; DB 1; Length 68;  
Best Local Similarity 38.2%; Pred. No. 14;  
Matches 13; Conservative 2; Mismatches 7; Indels 12; Gaps 3;

Qy 16 DPOTCKC----SCNNTDSRKAROLELNERTCRC 45  
Db 2 DPETCPGSGSGCTCAGDS-CKC-----EGCKC 27

RESULT 11  
US-07-924-063A-1  
Sequence 1, Application US/07924063A  
Patent No. 5489514  
GENERAL INFORMATION:  
APPLICANT: TSUJI, SHOJI; MIYATAKE, TADASHI; UCHIDA, YOKO;  
APPLICANT: IHARA, YASUO  
TITLE OF INVENTION: DNA CODING FOR GROWTH-INHIBITORY FACTOR AND  
TITLE OF INVENTION: USE THEREOF  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/924,063A  
FILING DATE: 19920828  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP91/01714  
FILING DATE: 13-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 410165/1990  
FILING DATE: 13-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: TSU-23  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-661-8000  
TELEFAX: 212-661-8002  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: Single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: human  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE: brain  
CELL TYPE:  
CELL LINE:

ORGANELLE:  
FEATURE:  
NAME/KEY: GIF  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-07-924-063A-1

Query Match 19.7% Score 52; DB 1; Length 68;  
Best Local Similarity 38.2% Pred. No. 14;  
Matches 13; Conservative 2; Mismatches 7; Indels 12; Gaps 3;

QY 16 DPOTKC-----SCKNTDSRCKAROLELNERC 45  
11:11 11 11 11  
DB 2 DPETCPGSGSGCTCADS-CKC-----EGCKC 27

RESULT 12  
US-08-138-340B-2  
Sequence 2, Application US/08138340B  
Patent No. 5538947  
GENERAL INFORMATION:  
APPLICANT: UCHIDA, YOKO; IHARA, YASUO  
TITLE OF INVENTION: GROWTH INHIBITORY FACTOR  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/138,340B  
FILING DATE: 18-OCT-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP/92/280201  
FILING DATE: 19-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP/92/346853  
FILING DATE: 25-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: TSU25  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68  
TYPE: Amino Acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-138-340B-2

Query Match 19.7% Score 52; DB 1; Length 68;  
Best Local Similarity 38.2% Pred. No. 14;  
Matches 13; Conservative 2; Mismatches 7; Indels 12; Gaps 3;

QY 16 DPOTKC-----SCKNTDSRCKAROLELNERC 45  
11:11 11 11 11  
DB 2 DPETCPGSGSGCTCADS-CKC-----EGCKC 27

RESULT 13  
US-08-726-306A-128  
Sequence 128, Application US/08726306A  
Patent No. 5958684  
GENERAL INFORMATION:  
APPLICANT: van Leeuwen, Frederik Willem  
APPLICANT: Burdach, Johannes Peter Henri  
APPLICANT: Grosveld, Franklin G.  
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: 1 Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,306A  
FILING DATE: 02-Oct-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 95/20080.4  
FILING DATE: 02-Oct-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,832  
FILING DATE: 01-Jan-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SRO ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-726-306A-128

Query Match 19.7% Score 52; DB 2; Length 97;  
Best Local Similarity 30.2% Pred. No. 20;  
Matches 13; Conservative 6; Mismatches 16; Indels 8; Gaps 2;

QY 2 CGPSEKRLHFDVDPOTKCSCCKNTDSRCKAROLELNERC 44  
1111 1111 1111 1111  
DB 37 CRPCASARA-----PRSCGASPPPTCASCVSASSAI-PMTCR 71

RESULT 14  
US-09-020-880-14  
Sequence 14, Application US/09020880A  
Patent No. 6136558  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ballinger, Marcus D.  
APPLICANT: Jones, Jennifer T.  
APPLICANT: Fairbrother, Wayne J.  
APPLICANT: Silkowski, Mark X.  
TITLE OF INVENTION: HERGULIN VARIANTS  
FILE REFERENCE: 14918-720CON1  
CURRENT APPLICATION NUMBER: US/09/020,880A  
CURRENT FILING DATE: 1998-02-09

; EARLIER APPLICATION NUMBER: US 60/037,581  
; EARLIER FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: No. 6136558 relevant (recombinant)  
US-09-020-880-14

Query Match 18.9%; Score 50; DB 4; Length 49;  
Best Local Similarity 31.6%; Pred. No. 17;  
Matches 12; Conservative 4; Mismatches 12; Indels 10; Gaps 2;

OY 5 CSERRKH-----LFVODPOTCKCCKN--TDSRCK 32  
1:1:1 1:1:1 1:1:1 1:1:1  
Db - 6 CAEKERTFCVNGGECFVWVKDPSRYLCKCPNEFTGDRQ 43

RESULT 15  
US-09-020-880-16  
; Sequence 16, Application US/09020880A  
; Patent No. 6136558  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ballinger, Marcus D.  
; APPLICANT: Jones, Jennifer T.  
; APPLICANT: Fairbrother, Wayne J.  
; APPLICANT: Sliwowski, Mark X.  
; APPLICANT: Wells, James A.  
; TITLE OF INVENTION: HEREGULIN VARIANTS  
; FILE REFERENCE: 14918-720CON1  
; CURRENT APPLICATION NUMBER: US/09/020,880A  
; CURRENT FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: US 60/037,581  
; EARLIER FILING DATE: 1997-02-10  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 49  
; TYPE: PRT  
; ORGANISM: No. 6136558 relevant (recombinant)  
US-09-020-880-16

Query Match 18.9%; Score 50; DB 4; Length 49;  
Best Local Similarity 31.6%; Pred. No. 17;  
Matches 12; Conservative 4; Mismatches 12; Indels 10; Gaps 2;

OY 5 CSERRKH-----LFVODPOTCKCCKN--TDSRCK 32  
1:1:1 1:1:1 1:1:1 1:1:1  
Db 6 CAEKERTFCVNGGECFVWVKDPSRYLCKCPNEFTGDRQ 43

Search completed: January 31, 2002, 11:21:27  
Job time: 138 sec

**THIS PAGE BLANK (USPTO)**